

STIC-Biotech/ChemLib

174939

From: Mertz, Prema
Sent: Tuesday, December 20, 2005 12:42 PM
To: STIC-Biotech/ChemLib
Subject: 10/789,251

Please search SEQ ID NO2 with protein databases.

Please search SEQ ID NO:26 with DNA databases.

Please search SEQ ID NO:2, 26 with US PG PUB databases.

Thanks.

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Searcher: _____
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Date Searcher Picked up: _____
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Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using SW model

Run on: December 24, 2005, 10:22:43 ; Search time 16 Seconds

(without alignments)
1058.384 Million cell updates/sec

Title: US-10-789-251-2

Perfect score: 910

Sequence: 1 MKASSLAFSLSAFYLLMT.....AVVKALGELDILLQWMEETE 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156.5	17.2	178	2 A38580	interleukin-10 pre
2	155	17.0	170	1 Q0852	BCRF1 protein - hu
3	155	17.0	175	2 I46591	interleukin 10 - p
4	147.5	16.2	179	2 A48558	interleukin 10 hom
5	144	15.8	178	2 A34853	interleukin-10 pre
6	136	14.9	178	2 JN0475	interleukin-10 pre
7	94.5	10.4	567	2 JC5538	Rab geranylgeranyl
8	94.5	10.4	567	2 A45977	Rab geranylgeranyl
9	93.5	10.3	809	2 S64594	probable beta-adap
10	85	9.3	140	2 F83128	probable transcrip
11	81.5	9.0	646	2 T33346	hypothetical prote
12	81	8.9	1062	2 S46367	protein kinase CDC
13	80	8.8	542	2 T19925	hypothetical prote
14	76.5	8.4	502	2 AD3160	hypothetical prote
15	76.5	8.4	553	2 B90153	2-isopropylmalate
16	76	8.4	523	2 S64826	probable membrane
17	76	8.4	917	2 T21870	hypothetical prote
18	75	8.2	276	2 B71517	probable synchocy
19	75	8.2	726	2 T46023	ATP-dependent RNA
20	75	8.2	729	2 H84912	probable pre-mRNA
21	74.5	8.2	121	2 B83640	hypothetical prote
22	74.5	8.2	1047	2 D71302	probable exonuclea
23	74	8.1	682	1 H69879	ATP-dependent DNA
24	73.5	8.1	449	2 B71917	udp-n-acetylmurama
25	73.5	8.1	653	2 D87602	sensory box histid
26	73.5	8.1	729	2 F97321	membrane export pr
27	73.5	8.1	782	2 S33945	late protein, 100K
28	73.5	8.1	794	2 A98211	hypothetical prote
29	73.5	8.1	794	2 C86057	hypothetical prote

ALIGNMENTS

RESULT 1
A38580
interleukin-10 precursor - human
N:Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10
C:Species: Homo sapiens (man)
C>Date: 14-Feb-1992 #sequence, revision 14-Feb-1992 #text change 09-Jul-2004
C/Accession: A38580; G01539; S49110; I37890
R/Vieira, P.; de Maal-Malefyt, R.; Dang, M.N.; Johnson, K.E.; Kastelein, R.; Florentin
Proc. Natl. Acad. Sci. U.S.A. 88, 1172-1176, 1991
A>Title: Isolation and expression of human cytokine synthesis inhibitory factor cDNA c
A:Reference number: A38580; MUID:91142134; PMID:1847510
A/Accession: A38580
A:Molecule type: mRNA
A:Residues: 1-178 <VIR>
A:Cross-references: UNIPROT:P22301; UNIPARC:UPI0000034E50; GB:M57627; NID:G186270; PID:
R:Windsor, W.T.; Syco, R.; Tsaribopoulos, A.; Zhang, R.; Durkin, J.; Baldwin, S.; Paliw
Biochemistry 32, 8807-8815, 1993
A>Title: Disulfide bond assignments and secondary structure analysis of human and mur.
A:Reference number: A48693; MUID:93372085; PMID:8364028
A:Contents: annotation; disulfide bonds in recombinant protein
R:Sanjanwala, B.
submitted to the EMBL Data Library, October 1994
A:Reference number: G07695
A/Accession: G01539
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-178 <SAN>
A:Cross-references: UNIPARC:UPI0000034E50; EMBL:U16720; NID:G1041012; PIDN:AAA80104.1;
R:Rube, D.; Platzter, C.; von Knechten, A.; Straub, H.; Hafner, M.; Tesch, H.
submitted to the EMBL Data Library, March 1994
A:Description: Isolation of the human interleukin-10-promoter. Characterization of the
A:Reference number: S49110
A/Accession: S49110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6, 'PVAWS' <KUB>
A:Cross-references: UNIPARC:UPI0000178477; EMBL:X78437; NID:G1167482
R:Platzter, C.; Volk, H.D.; Platzter, M.
DNA Seq. 4, 399-401, 1994
A>Title: 5' noncoding sequence of human IL-10 gene obtained by oligo-cassette PCR walk
A:Reference number: I37890; MUID:95143580; PMID:7841462
A/Accession: I37890
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <PLA>
A:Cross-references: UNIPARC:UPI000011B9B9; EMBL:X73536; NID:G452395; PIDN:CAA51942.1;
C:Genetics: GDB:IL10, IL-10
A:Gene: GDB:IL10, IL-10
A:Cross-references: GDB:128636; OMIM:124092
A:Map position: 1q31-1q32
A:introns: 55/3; 75/3; 126/3; 148/3
C:Superfamily: interleukin-10

N/Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10
 C/Species: Mus musculus (house mouse)
 C/Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
 A/Accession: A34853; 156136
 R/Moore, K.W.; Vieira, P.; Florentino, D.F.; Trounstein, M.L.; Khan, T.A.; Mosmann, T.R.
 Science 248, 1230-1234, 1990
 A/Title: Homology of cytokine synthesis inhibitory factor (IL-10) to the Epstein-Barr vA
 A/Reference number: A34853; MUID:90273182; PMID:2161559
 A/Accession: A34853
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-178 <MO>
 A/Cross-references: UNIPROT:P18893; UNIPARC:UPI000002149E; GB:M37897; NID:G198286; PIDN:
 J.Kim, J.M.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Khan, T.A.; Moore, K.W.
 R. Immunol. 148, 3618-3623, 1992
 A/Title: Structure of the mouse IL-10 gene and chromosomal localization of the mouse and
 A/Reference number: 156136; MUID:92268508; PMID:1350294
 A/Accession: 156136
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-178 <RES>
 A/Cross-references: UNIPARC:UPI000002149E; GB:M84340; NID:G198291; PIDN:AAA39275.1; PID:
 C/Genetics:
 A/Gene: IL10
 A/Intons: 55/3; 75/3; 126/3; 148/3
 C/Superfamily: Interleukin-10
 C/Keywords: cytokine; lymphokine; T-cell

Query Match 15.8%; Score 144; DB 2; Length 178;
 Best Local Similarity 31.1%; Pred. No. 1.3e-06;
 Matches 42; Conservative 19; Mismatches 68; Indels 6; Gaps 4;

QY 39 LOEIRNGFSIDRSGVAKDGNIDIRILRRTESLQDTKPARCCLRLRLYLDRYFKNY 98
 DB 41 LLELRTRAFSQVKTFPQKD-QLD-NILTDLSLMDDFGYGCGALSEMTQFYLVEMPOA 98
 QY 99 QTPDHYTLRKISLANSFLTIKDLRLCHAMTCHGCEAMKRYQSILSHFEKLEPOAAV 158
 DB 99 EKKGPEIKHLNLSGELKTLRLRRLRCHRFPC---ENSKAVQVQKSPNLTQDQ-GV 154
 QY 159 VKALGELDILQWME 173
 DB 155 YKANMEFDIFINCIE 169

RESULT 6
 JN0475
 N/Alternate names: cytokine synthesis inhibitory factor
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 A/Accession: JN0475; JCI357; S36021
 R/Feng, L.; Tang, W.W.; Chang, J.C.C.; Wilson, C.B.
 Biochem. Biophys. Res. Commun. 192, 452-458, 1992
 A/Title: Molecular cloning of rat cytokine synthesis inhibitory factor (IL-10) cDNA and
 A/Reference number: JN0475
 A/Accession: JN0475
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-178 <FEN>
 A/Cross-references: UNIPROT:P29456; UNIPARC:UPI0000167959
 R/Goodman, R.E.; Oblak, J.; Bell, R.G.
 Biochem. Biophys. Res. Commun. 189, 1-7, 1992
 A/Title: Synthesis and characterization of rat interleukin-10 (IL-10) cDNA clones from
 A/Reference number: JCI357; MUID:93080542; PMID:1280414
 A/Accession: JCI357
 A/Molecule type: mRNA
 A/Residues: 1-178 <GOO>
 A/Cross-references: UNIPARC:UPI000012D477; GB:I02926; NID:G204903; PIDN:AAA41425.1; PID:
 R/Feng, L.
 submitted to the EMBL Data Library, July 1991
 A/Reference number: S36021
 A/Accession: S36021

A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-178 <FE2>
 A/Cross-references: UNIPARC:UPI0000167959; EMBL:X60675; NID:G296620; PIDN:CAA43090.1;
 C/Superfamily: Interleukin-10
 C/Keywords: cytokine; glycoprotein; lymphokine; T-cell
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-178/Product: interleukin-10 #status predicted <MAT>
 F;29,134/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.9%; Score 136; DB 2; Length 178;
 Best Local Similarity 28.5%; Pred. No. 8e-06;
 Matches 53; Conservative 26; Mismatches 77; Indels 30; Gaps 8;

QY 1 MKRASSLAFSLSAAFILMTPTSTGLKTLNLSGVATN-----LOEIRNGFSD 48
 DB 1 MGSALICLLLIA-----GVKT-SKSHSIRGDNCTHFPVSQTHLRRLRAFSQ 50
 QY 49 IRGSVQAKDGNIDIRILRRTESLQDTKPARCCLRLRLYLDRYFKNYQTPDHYTLR 107
 DB 51 VKTFPQKD-QLDNIVL--TDSLQDFKGLGCGALSEMTKPYLVEMPOAENHGPRIKE 107
 QY 108 KISSLANSFLTIKDLRLCHAMTCHGCEAMKRYQSILSHFEKLEPOAAVVKALGELDT 167
 DB 108 HINSLGEKLTLMILQRCHRFPC---ENSKAVQVQKNDPKNLQDK-GVYKANMEFDI 163
 QY 168 LQWME 173
 DB 164 FINCIE 169

RESULT 7
 JCS538
 Rab geranyl transferase (EC 2.5.1.-) alpha chain - human
 C/Species: Homo sapiens (man)
 C/Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
 A/Accession: JCS538
 R/Song, H.J.; Rossi, A.; Cecil, R.; Kim, I.G.; Anzano, M.A.; Jang, S.I.; De Laurenzi, V.
 Biochem. Biophys. Res. Commun. 225, 10-14, 1997
 A/Title: The genes encoding geranyl transferase alpha-subunit and transglutamin
 A/Reference number: JCS538; MUID:97339427; PMID:9196026
 A/Accession: JCS538
 A/Molecule type: DNA
 A/Residues: 1-567 <SON>
 A/Cross-references: UNIPROT:Q92696; UNIPARC:UPI000013188E
 C/Comment: This protein is involved in cutaneous disease. The gene of this enzyme is p
 C/Genetics:
 A/Gene: Rabggtc
 A/Intons: 1/3; 38/3; 81/1; 143/1; 211/1; 238/2; 278/3; 300/3; 336/2; 354/2; 383/2; 41
 C/Keywords: transferase

Query Match 10.4%; Score 94.5; DB 2; Length 567;
 Best Local Similarity 25.8%; Pred. No. 0.35;
 Matches 49; Conservative 26; Mismatches 82; Indels 33; Gaps 9;

QY 1 MKRASSLAFSLSAAFILMTPTSTGLKTLNLSGVATNQE--IRNGFSD---IRGSVQA 55
 DB 304 LPAASLNDQLPQHTFVIVTADYOK----BCVLKGRQEGCRDSTDEQLFRCLELV 358
 QY 56 KQGNIDIRILRRTESLQDTKPARCCLRLRLYLDRYFKNYQTPDHYTLR 103
 DB 359 EKSTVQSLBESCKELQELPEKWKCLTITILMRALDPLVEKETLYQFOTLKAVDPKR 418
 QY 104 YT---LKKISSLANSFLTIK---KDLRLCHAMTCHGCEAMKRYQSILSH--FEKL 152
 DB 419 ATYLDLRSKFTLENSVLKGEYAEVAVLHAKDLTLVCLHLEGLLVTHLDLSHNRRLRL 478
 QY 153 EQQAAVVKL 162
 DB 479 PALAALRCL 488

RESULT 8

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A45977
Rab geranylgeranyl transferase component B alpha subunit - rat
C|Species: Rattus norvegicus (Norway rat)
C|Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C|Accession: A45977
R|Armstrong, S.A.; Seabra, M.C.; Sudhof, T.C.; Goldstein, J.L.; Brown, M.S.
J| Biol. Chem. 268, 12221-12229, 1993
A|Title: cDNA cloning and expression of the alpha and beta subunits of rat Rab geranylge
A|Reference number: A45977; MUID:93280201; PMID:8505342
A|Accession: A45977
A|Status: preliminary
A|Molecule type: mRNA; protein
A|Residues: 1-567 <ARM>
A|Cross-references: UNIPROT:Q08602; UNIPARC:UPI000013188F; GB:S62096; NID:g385474; PIDN:
A|Experimental source: brain
A|Note: sequence extracted from NCBI backbone (NCBIN:133369, NCBIP:133370)

Query Match      10.4%; Score 94.5; DB 2; Length 567;
Best Local Similarity 24.1%; Pred. No. 0.35;
Matches 46; Conservative 31; Mismatches 80; Indels 33; Gaps 8;

OY 1 MKASSIAFSILSAAYLLMTPTGTGLKTLNLGSCVATNMLOE--IRNGSD--IRGSVOA 55
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB LPAASINDLPQHTFRIRWTGSDSQ-----ECVILKORPEWCGRDSATDEGLPFCELSV 358
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 56 KGNINDIRIIRTRESLDOTYPANRCCLIRHLRL-YDVRFPKNQTDPHYT----- 105
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 359 EKSTVLQSELESCKELDELPEPKLCITILLMRALDPLLYEKETLQFYSLKAVDPMR 418
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 106 -----LRKISSLANSLFTLK---KDRLGHAMHNTCHGSEAMKKYSQI-LSH--FEEL 152
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 419 AAVLDLRSKFLENSVLKMEYADVRLVHLAHKDLTVLCHLEQLLVTHLDISHNRRLAL 478
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 153 EPOAAVVKAL 162
    |||:|||:
DB 479 PRLAALARCL 488

RESULT 9
S64594
Probable beta-adaptin YKS5 - Yeast (Saccharomyces cerevisiae)
N|Alternate names: protein G93j1; protein YGR261c
C|Species: Saccharomyces cerevisiae
C|Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
R|Panzerl, U.; Agostoni Carbone, M.L.; Melchioretto, P.; Plevani, P.; Martegani, E.; Var
submitted to the Protein Sequence Database, May 1996
A|Reference number: S64591
A|Accession: S64594
A|Cross-references: UNIPROT:P46682; UNIPARC:UPI00000530A8; EMBL:Z73046; NID:g1323474; PI
A|Residues: 1-809 <PAN>
A|Molecule type: DNA
A|Cross-references: UNIPROT:P46682; UNIPARC:UPI00000530A8; EMBL:Z73046; NID:g1323474; PI
A|Experimental source: strain S288C
R|Robinson, U.C.; Engle, H.M.; Panek, H.R.
submitted to the EMBL Data Library, September 1995
A|Description: Suppressors of loss of yeast casein kinase 1 function define the four sub
A|Reference number: S63439
A|Accession: S63450
A|Cross-references: UNIPARC:UPI0000168A41; EMBL:U35411; NID:g1017728; PID:g1017729
A|Molecule type: DNA
A|Residues: 1-26; 'PLSWNPV', 36-723, 'T', 725-795, 801-809 <ROB>
A|Cross-references: UNIPARC:UPI0000168A41; EMBL:U35411; NID:g1017728; PID:g1017729
C|Genetics:
A|Gene: SGD:YKS5
A|Cross-references: SGD:S0003493; MIPS:YGR261c
A|Map position: 7R

Query Match      10.3%; Score 93.5; DB 2; Length 809;
Best Local Similarity 24.1%; Pred. No. 0.66;
Matches 48; Conservative 39; Mismatches 73; Indels 39; Gaps 10;

OY 2 KASSLAFLSLISAAYLLMTPTGTGLKTLNLGSCVATNMLOEIRNGSDIRGSGVQADGNID 61
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 21 EAAVAVTSTKGESYYTY--SQINPPOOLVTLNLSRNREVDAMKRITISINASDDSD:ID 78

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Qy      62 IRI-----LRRESIQDTPRPARCCLRLHLRLYLVDYFQKYNQGTGDHITLKRISSLANSL 117
      79 VOLYFADYVKNITNTDTR-----VRKILLYLRLPRN---DPNLTLSINSLQSL 128
Db      118 TIKDQLRLCHAHMTCGGEAMKKYSQILSHPEK---LEPOA-----AVK--ALGE 164
      129 DSNSELR-CFA--LSALSDMKSSSLAPILHTVTKVLTDPFAMVRGEVALAIITLYRAGK 185
Qy      165 -----LDITLQWMEETE 176
      186 NDYHEELDITLKELMADTD 204
Db

RESULT 10
F83128
Probable transcription regulator PA4135 [imported] - Pseudomonas aeruginosa (strain PAO
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F83128
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laidig, K.; Lim
, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83128
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <STD>
A:Cross-references: UNIPROT:Q9HWP6; UNIPARC:UPI00000C5C2C; GB:AE004830; GB:AE004091; NI
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA4135

Query Match      9.3%; Score 85; DB 2; Length 140;
Beet Local Similarity 24.5%; Pred. No. 0.56;
Matches 25; Conservative 25; Mismatches 42; Indels 10; Gaps 3;

Qy      62 IRIIRRESLODTPRPARCCILRL-----LRLYLDRFVKNYQTPDHTTLKRISSLANSL 115
      40 IRIIRQOGEMESYGLANQACTLRPSMTGVLARLRDGIVRKAKPKQOR-RVYVNLTEKG 98
Db      116 --FLTIKDQLRLCHAHMTCGGEAMKKYSQILSHPEKLEP 154
      99 QQCFVSMGDMEXKYNQRIQERFGEKLAQLLELNLKIKP 140
Db

RESULT 11
T33346
Hypotheetical protein C16A11.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33346
R:Johnson, D.; Blewaid, T.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of C. elegans cosmid C16A11.
A:Reference number: Z21328
A:Accession: T33346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-646 <JOH>
A:Cross-references: UNIPROT:O76579; UNIPARC:UPI0000076553; EMBL:AF077536; PIDN:AAC26261
A:Experimental source: strain Bristol N2; clone C16A11
C:Genetics:
A:Gene: CESP:C16A11.5
A:Map position: 2
A:Introns: 35/3; 72/1; 94/3; 129/3; 184/3; 205/1; 279/3; 387/3; 505/2; 540/2; 570/3

Query Match      9.0%; Score 81.5; DB 2; Length 646;
Beet Local Similarity 26.1%; Pred. No. 7.5;
Matches 36; Conservative 22; Mismatches 49; Indels 31; Gaps 8;

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QY 29 NLSQCVATNLOEIRNGFSDINGSOAKOGNIDILK-----RRESIQDTKPNARC 80
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 176 NQACAFVDSLEQ-RNSNGDHLPIVQELDSMKSIFFIPIQAKHKAVPIEDLKPSYC 234
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 81 CL-LRHLLRLRYLD-----RVPKNYQTPD--HYTLKRISLANSFLTIKQDLCHAMTC 132
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 235 ILAVDALFELFENETINGSRVFEHGKPIIEYVL-KIPL----LLFKSELRLPHPIKTA 288
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 133 HCGEBAMKKYSQILSHFE 150
      |:::|:::|
Db 289 H-----LHRLLASFE 298

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RESULT 12

protein kinase CDC7 (EC 2.7.1.1) - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 05-Oct-2004
C:Accession: S46367, T39888
R:Frankhauser, C.; Simanis, V.
EMBO J. 13, 3011-3019, 1994
A:Title: The cdc7 protein kinase is a dosage dependent regulator of septum formation in
A:Accession: S46367, MUID:94313982, PMID:8039497
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-1062 <PAN>
A:Cross-references: UNIPROT:P41892; UNIPARC:UPI0000127259; EMBL:X78799; NID:G521098; PIR
A:Experimental source: wildtype 972 h minus
A:Note: mRNA sequencing was also done to confirm the intron borders
R:Sanders, D.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, February 1995
A:Reference number: Z21860
A:Accession: T39888
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1062 <SUA>
A:Cross-references: UNIPARC:UPI0000127259; EMBL:AL035537; PIDD:CA83686.1; GSPDB:GN00067
A:Experimental source: strain 972h-, cosmid c21
A:Gene: CDC7, SPDB:SPBC21.06c
A:Map position: II, 2
A:Insertions: 9/3; 54/3; 64/3; 86/2; 171/1; 325/1; 405/3; 427/1; 544/3; 589/3
C:Function:
A:Description: essential for septum formation and cell division
C:Keywords: ATP; cell division; phosphotransferase; protein kinase
F:7-259/Domain: protein kinase homology <KIN>
F:15-23/Region: protein kinase ATP-binding motif

```

Query Match      8.9%; Score 81; DB 2; Length 1062;
Best Local Similarity 30.2%; Pred. No. 15;
Matches 32; Conservative 20; Mismatches 44; Indels 10; Gaps 4

QY      23 TGLKTLNLGSCVATNTLQLRNG-PSDIRGVSQAQKGNIDIRILRFTESLDQTPANRCC 81
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      466 TGLGTLVLWKCYGSWMNEENEDGESDIDFSIETLLEMLDIE-----NNIALDKRTILAS 520
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      82 LLEHLRLVLDLRFKNYQTFPDHYTLRKISLSLANSFLTKKDLRLCH 127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      521 LLSLGLGSLRD--KNIGSKD-TTVSQINSLISELSDUKREIRIQAH 562
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
T19925
hypothetical protein C44C10.4 - Caenorhabditis elegans
C|Species: Caenorhabditis elegans
C|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text change 09-Jul-2004
C|Accession: T19925
R|Cottage, A.
submitted to the EMBL Data Library, February 1996
A|Reference number: Z19197
A|Accession: T19925
A|Status: preliminary; translated from GB/EMBL/DBJ

```

A:Molecule type: DNA
A:Residues: 1-542 <WIL>
A:Cross-references: UNIPROT:O18616, UNIPARC:UPI000017B837, EMBL:Z69787, PIDD:CA93638.
A:Experimental source: clone C44C10
C:Genetics:
A:Gene: CESP:C44C10.4
A:Map position: X
A:Introns: 66/3, 229/3, 309/1, 328/3, 398/3

Query Match	8.8%;	Score 80;	DB 2;	Length 542;
Best Local Similarity	23.2%;	Pred. No. 8.5;		
Matches 29;	Conservative 25;	Mismatches 43;	Indels 28;	Gaps 4;

```

QY 39 LOEIRNGFDINGSVQAKDGNIDIRLRRTSLDQTPKARCCLRLRLRYLDRVFKNY 98
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 212 IOETKEKFAEOLKVNNAKNAKMPILSIYSSEAIPIKQTPSPN-----PKNN 256
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 99 -----QTPDHY----TLRKISLSLANSFLTIKKOL--RLCHAWTCHCGEAMKRYSOI 145
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 AIYVRPKTNHNDLITVDKLSYINERKETERRELOFAVNHPMNIRFSEBGNIIYARE 316
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 146 LSHFE 150
    : : : |
Db 317 IDYTE 321

```

RESULT 14

hypothetical protein glnP/glnQ [imported] - Agrobacterium tumefaciens (strain C58, [download](#))
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #ext_change 09-Jul-2004
C:Accession: AD3160
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.;
erage, G.; Gillet, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCle,
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference numbers: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD3160
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-502 <KUR>
A:Cross-references: UNIPROT:O9WWF4; UNIPARC:UPI00000D146D; GB:AE008687; PIDN:AA145698.
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: glnP/glnQ
A:Genome: plasmid

Query Match	8.4%;	Score 76.5;	DB 2;	Length 502;
Best Local Similarity	24.6%;	Pred. No. 17;		
Matches 42;	Conservative 23;	Mismatches 37;	Indels 69;	Gaps 10;

[illegible]

RESULT 15

2-isopropylmalate synthase, probable [leuA-1] [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: B90153

R,She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R. arett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.

Submitted to Genbank, April 2001

A/Description: Sulfolobus solfataricus complete genome.

A/Reference number: A99139

A/Accession: B90153

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1553 <RIR>

A/Cross-references: UNIPROT:Q98021; UNIPARC:UP100000641BD; GB:AE006641; NID:g13813259; E

C/Genetics:

A/Gene: leuA-1

C/Superfamily: 2-isopropylmalate synthase leuA

Query Match 8.4%; Score 76.5; DB 2; Length 553;

Best Local Similarity 19.6%; Pred. No. 19;

Matches 39; Conservative 34; Mismatches 61; Indels 65; Gaps 8;

```

QY 24 GLKTLNLSGCVIATNLOETNGFSDIRGSVQA---KQGNID-----IRILRR 67
Db 232 GTHANDIGCAVANSIMATAGARHVQGTINGIGERTGNADLIQIITLILKKGGLNALNG 291
QY 68 TESLODTKPPAMRCC-----LIRHLRLYLDRVFNKYQTPDH----- 103
Db 292 QESLRKLRREVSRIYVEILGLPPNPQPYVGDNAPAHKAGVHDVAVKVPRAVEHVDPSLV 351
QY 104 ----YTLRKISLAN--SFL-----TIKIDRLCHAHNTCHGEBAMKKYSQILSHPE 150
Db 352 GNDREKVISLSTGANLVSYLGLGIAVDKDERL-----KKALNKIKELERAGY 401
QY 151 KLE--POAAVVKALGELDI 167
Db 402 SPDVGPASATLITLKEIINT 420

```

Search completed: December 24, 2005, 10:28:05
Job time : 18 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 24, 2005, 10:26:03 ; Search time 228 Seconds

(without alignments)
544.618 Million cell updates/sec

Title: US-10-789-251-2

Perfect score: 910

Sequence: 1 MKASSLAFSLGSAFYLLWT.....AVKALGELDILLQMMETE 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	906	99.6	176	1 IL10_HUMAN	09NYV1 homo sapien
2	672	73.8	176	1 IL10_MOUSE	09JXV1 mus musculi
3	337.5	37.1	177	1 IL19_HUMAN	09UD0 homo sapien
4	337.5	37.1	215	2 O5VUT3_HUMAN	05VUT3 homo sapien
5	306	33.6	168	2 O4LDR4_BRAE	04LDR4 brachydanto
6	281.5	30.9	176	1 IL19_MOUSE	08CJ70 mus musculi
7	266.5	29.3	175	2 O7SK60_TETNG	07SK60 tetradon n
8	222	24.4	220	2 O92SJ3_MOUSE	092SJ3 mus musculi
9	220	24.4	181	2 O92S54_MOUSE	092S54 mus musculi
10	217	23.8	206	1 IL24_HUMAN	013007 homo sapien
11	217	23.8	207	2 O53XZ7_HUMAN	053XZ7 homo sapien
12	191	21.0	183	2 O9WV8_RAT	09WV8 rattus norv
13	187	20.5	183	2 O6A2H5_CHICK	06A2H5 gallus gall
14	175.5	19.3	175	2 O6A2H4_CHICK	06A2H4 gallus gall
15	175.5	19.3	175	2 O6A2H4_CHICK	06A2H4 gallus gall
16	161.5	17.7	178	1 IL10_MACNE	08UJ36 cercopithec
17	161	17.7	177	2 O8UJ36_MACNE	08UJ36 cercopithec
18	157.5	17.3	178	1 IL10_MACNE	08UJ36 cercopithec
19	157.5	17.3	178	1 IL10_MACNE	08UJ36 cercopithec
20	157.5	17.3	178	1 IL10_MACNE	08UJ36 cercopithec
21	157.5	17.3	178	1 IL10_MACNE	08UJ36 cercopithec
22	156.5	17.2	160	2 O7I3I1_CYPRA	07I3I1 cyprinus ca
23	156.5	17.2	178	1 IL10_FELCA	07I3I1 cyprinus ca
24	156.5	17.2	178	1 IL10_FELCA	07I3I1 cyprinus ca
25	156.5	17.2	178	1 IL10_FELCA	07I3I1 cyprinus ca
26	155	17.0	170	2 O6FGM4_HUMAN	06FGM4 homo sapien
27	155	17.0	170	2 O6FGM4_HUMAN	06FGM4 homo sapien
28	155	17.0	170	2 O6FGM4_HUMAN	06FGM4 homo sapien
29	154.5	17.0	175	1 IL10_PIG	0777H2 equus caball
30	153	16.8	178	1 IL10_CERTO	0777H2 equus caball
31	151.5	16.6	179	1 IL10_CEREL	0777H2 equus caball

32	151	16.6	178	1 IL10_RABIT	09EJ14 oryctolagus
33	147.5	16.2	178	2 O9TWD3_RABIT	09TWD3 oryctolagus
34	147.5	16.2	179	1 IL10H_EBV2	P68678 equine herp
35	147.5	16.2	179	1 IL10H_EBV2	P68678 equine herp
36	147	16.2	178	1 IL10_MOUSE	P18933 mus musculi
37	145.5	15.9	160	2 O6FGS9_HUMAN	06FGS9 mus musculi
38	144.5	15.9	160	2 O923T1_SIGHI	0923T1 sigmodon hi
39	144.5	15.9	174	1 IL10_TFIVU	097798 trichosurus
40	144.5	15.9	178	1 IL10_HORSE	028374 equus caball
41	143.5	15.8	178	2 O6VW71_BUBBU	06VW71 bubalus bub
42	143	15.7	171	2 O9Q5L1_CHY12	09Q5L1 cercopithec
43	142.5	15.7	178	1 IL10_BOVIN	P43480 bos taurus
44	142.5	15.7	178	2 O8MK99_SALISC	08MK99 salmtr sci
45	142	15.6	181	1 IL10_CANPA	P48411 canis fami

ALIGNMENTS

RESULT 1
IL10_HUMAN STANDARD; PRT; 176 AA.
AC O9NYV1; O96Q26;
ID IL10_HUMAN
DT 28-FEB-2003 (Rel. 41, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin-20 precursor (IL-20) (four alpha helix cytokine Zcyto10).
GN Name=IL20; Synonyms=ZCYT10; ORFNames=UN0852/PRO1801;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21097717; PubMed=1163236; DOI=10.1016/S0092-8674(01)00187-8;
RA Blumberg P.M., Conklin D., Xu W.F., Grossmann A., Brenner T.,
RA Carroll S., Egan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
RA Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA Prunkard D., Saxon S., Sprecher C., Waggle K., West J.,
RA Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekhar Y.A.;
RT "interleukin 20: discovery, receptor identification, and role in
RT epidermal function.";
RL Cell 104:9-19(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Peol C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattlesNPE, NHLBI HL66682 program for genomic applications, UW-
RT FRRC, Seattle, WA (URL: <http://pga.ge.washington.edu>).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBD databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Bush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Helene S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbe E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandenberg R.L., Watanabe C., Wiand D., Woods K., Xie M.-H.,
RA Yanura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Goddard P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.D., Feinold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska A., Smallos D.E.,
 RA Schenker A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP PROTEIN SEQUENCE OF 25-39.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.,
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 CC -1- FUNCTION: Cytokine that may be involved in epidermal function and
 CC proinflamm. Acts through STAT3.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed at very low levels in skin, trachea,
 CC and other tissues.
 CC -1- SIMILARITY: Belongs to the IL-10 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL, AF224266; AAF36579.1; -; mRNA.
 DR EMBL, AF402002; AAK84423.1; -; Genomic DNA.
 DR EMBL, AY358320; AAG8686.1; -; mRNA.
 DR EMBL, BC069311; AAH69311.1; -; mRNA.
 DR EMBL, BC069364; AAH69364.1; -; mRNA.
 DR EMBL, BC069398; AAH69398.1; -; mRNA.
 DR EMBL, BC069425; AAH69425.1; -; mRNA.
 DR EMBL, BC069449; AAH69449.1; -; mRNA.
 DR EMBL, BC069487; AAH69487.1; -; mRNA.
 DR EMBL, BC069523; AAH69523.1; -; mRNA.
 DR EMBL, BC069559; AAH69559.1; -; mRNA.
 DR EMBL, BC074948; AAH74948.1; -; mRNA.
 DR EMBL, BC074949; AAH74949.1; -; mRNA.
 DR HSSP, Q9UHD0, INIF.
 DR Ensemble, ENSG00000162891; Homo sapiens.
 DR HGN, HGNC:6002, IL20.
 DR MIM, 605619; -.
 DR GO, GO:0005576; C:extracellular region; TAS.
 DR GO, GO:0045517; F:interleukin-20 receptor binding; TAS.
 DR GO, GO:0030097; P:nemopoiesis; ISS.
 DR GO, GO:0045606; P:positive regulation of epidermal cell diffe. . .; TAS.
 DR GO, GO:0045618; P:positive regulation of keratinocyte diffe. . .; TAS.
 DR GO, GO:0042517; P:positive regulation of tyrosine phosphoryla. . .; TAS.
 DR GO, GO:0050727; P:regulation of inflammatory response; TAS.
 DR InterPro, IPR012351; Cytokine 4 hlx.
 DR InterPro, IPR012352; IL-10 add. helix.
 DR InterPro, IPR000098; Interleukin_10.
 DR Pfam, PF00726; IL10; 1.
 DR Prodom, PD003687; Interleukin_10; 1.
 DR PROSITE, PS00520; INTERLEUKIN_10; 1.
 KM Cytokine, Direct protein sequencing; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 176 Interleukin-20.
 FT DISULFID 33 126 Potential.
 FT DISULFID 80 132 Potential.
 FT DISULFID 81 134 Potential.

FT CONFLICT 48 48 E -> D (in Ref. 1).
 FT CONFLICT 126 126 C -> S (in Ref. 3).
 SQ SEQUENCE 176 AA; 20072 MW; 838592500B6C447 CRC64;
 Query Match 99.6%; Score 906; DB 1; Length 176;
 Best Local Similarity 99.4%; Pred. No. 1,8e-80;
 Matches 175; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKASSLAFSLNAAPFLMTPTSTGLKTLNLGSCVATNTQETRNQSDIRGSVQADGNT 60
 DB 1 MKASSLAFSLNAAPFLMTPTSTGLKTLNLGSCVATNTQETRNQSDIRGSVQADGNT 60
 QY 61 DRIIRRTSLQDTPRANRCCLRHLLRLYLDRVFKNQYOTPPHYTRKISSLSANSELTJK 120
 DB 61 DRIIRRTSLQDTPRANRCCLRHLLRLYLDRVFKNQYOTPPHYTRKISSLSANSELTJK 120
 QY 121 KDLRLCHAMTCHCEBANKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
 DB 121 KDLRLCHAMTCHCEBANKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
 RESULT 2
 IL20 MOUSE STANDARD; PRT; 176 AA.
 ID IL20 MOUSE
 AC 09UKV9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-20 precursor (IL-20) (Four alpha helix cytokine ZCYT010).
 GN Name=IL20; Synonyms=Zcyto10;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;
 RA Blumberg P., Conklin D., Xu W.F., Grossmann A., Brendler T.,
 RA Carroll S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
 RA Jellinek L., Kelly J.D., Madden K., Maurer M.P., Parfith-Novak J.,
 RA Punkard D., Saxon S., Sprecher C., Wagie K., West J.,
 RA Whitmore T.E., Yao L., Kuehle M.K., Dale B.A., Chandrasekhar Y.A.,
 RT "Interleukin 20: discovery, receptor identification, and role in
 RT epidermal function.";
 RL Cell 104:9-19(2001).
 CC -1- FUNCTION: Cytokine that may be involved in epidermal function and
 CC proinflamm. Acts through STAT3.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-10 family.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL, AF224267; AAF36680.1; -; mRNA.
 DR HSSP, Q9UHD0, INIF.
 DR Ensemble, ENSMUSG0000026416; Mus musculus.
 DR MGI, MGI:1890473; IL20.
 DR GO, GO:0005615; C:extracellular space; TAS.
 DR GO, GO:0045517; F:interleukin-20 receptor binding; IDA.
 DR GO, GO:0030097; P:nemopoiesis; NAS.
 DR GO, GO:0045606; P:positive regulation of epidermal cell diffe. . .; ISS.
 DR GO, GO:0045618; P:positive regulation of keratinocyte diffe. . .; ISS.
 DR GO, GO:0042517; P:positive regulation of tyrosine phosphoryla. . .; ISS.
 DR GO, GO:0050727; P:regulation of inflammatory response; ISS.
 DR InterPro, IPR012351; Cytokine 4 hlx.
 DR InterPro, IPR000098; Interleukin_10.
 DR Pfam, PF00726; IL10; 1.
 DR Prodom, PD003687; Interleukin_10; 1.

DR SMART; SM00188; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN_10; 1.
 KW Cytokine; Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 176 Interleukin-20.
 FT DISULFID 33 126 Potential.
 FT DISULFID 80 132 Potential.
 FT DISULFID 81 134 Potential.
 SQ SEQUENCE 176 AA; 20098 MW; 08577AF656574771 CRC64;
 Query Match 73.8%; Score 672; DB 1; Length 176;
 Best Local Similarity 75.3%; Pred. No. 1.5e-57;
 Matches 131; Conservative 15; Mismatches 28; Indels 0; Gaps 0;
 QY 1 MASSIASFLSLAAFLYLTPTSTGKTLNLGSCVATNLOEIRNGFSIDRSGVQAKDGN 60
 DB 1 MGFGLAFGLFSAVGLWLTPTLGLTKTLHSGCVATNLOAKERSEIRDSVQAKDNI 60
 QY 61 DIRILRTESLDPTKPNRCLRLHLRLYLDRVFKNYOTPHYTLRKISLANSFLTIK 120
 DB 61 DIRILRTESLDISLDRCCFLRLVRFYLDVRFVYOTPHHTLRKISLANSFLTIK 120
 QY 121 KDLRLCHAMTCHGSEAMKRSQIISHEKLEPQAAVVKALGELDILLQMMEE 174
 DB 121 KDLVCHSHMACGCEAMEKYNQIISHFIELELQAAVVKALGELGILLRMMEE 174
 RESULT 3
 IL19_HUMAN STANDARD; PRT; 177 AA.
 AC Q9UHD0; Q960R4; Q9NUA0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-MAY-2003 (Rel. 47, Last sequence update)
 DE Interleukin-19 precursor (IL-19) (Melanoma differentiation associated
 DE protein-like protein) (NG.1).
 GN Name=IL19; Synonyms=ZMDA1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RX MEDLINE=21040165; PubMed=1196675; DOI=10.1038/sj.gene.6363714;
 RA Gallagher G., Dickenshees H., Eskdale J., Izotova L.S.,
 RA Mitrochitchenko O.V., Peat J.D., Vasquez N., Donnelly R.P.,
 RA Kortenko S.V.;
 RT "Cloning, expression and initial characterization of interleukin-19
 RT (IL-19), a novel homolog of human interleukin-10 (IL-10).";
 RL (IL-19), a novel homolog of human interleukin-10 (IL-10).";
 RL Genes Immun. 1:442-450(2000).
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=22257669; PubMed=12370360;
 RX Liao Y.-C., Liang W.G., Chen F.W., Hsu J.H., Yang J.J., Chang M.-S.;
 RA "IL-19 induces production of IL-6 and TNF-alpha and results in cell
 RT apoptosis through TNF-alpha.";
 RL J. Immunol. 169:4288-4297(2002).
 RN NUCLEOTIDE SEQUENCE.
 RP Conklin D., Petersen J., Loften-Day C., Whitmore T., Muerer M.,
 RA Sexson S., Smith D., Lok S., Powder T., O'Hara P.;
 RT "Homo sapiens homolog of melanoma differentiation associated gene.";
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RP Kortenko S.V., Peatka S.;
 RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA), AND VARIANT PHE-175.
 RA Rieger M.J., Carington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattleSNPs. NHBLI HL66682 program for genomic applications, UW-

RT FHCRG, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP Human chromosome 1 international sequencing consortium;
 RG Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN PROTEIN SEQUENCE OF 25-39.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.U.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 RN X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 19-177, AND DISULFIDE BONDS.
 RX PubMed=12403790; DOI=10.1074/jbc.M208602200;
 RA Chang C., Magracheva E., Kozlov S., Fong S., Tobin G., Kortenko S.,
 RA Wlodawer A., Zdanov A.;
 RT "Crystal structure of interleukin-19 defines a new subfamily of
 RT helical cytokines.";
 RL J. Biol. Chem. 278:3308-3313(2003).
 CC -1- FUNCTION: May play some important roles in inflammatory responses.
 CC -1- UP-regulates IL-6 and TNF-alpha and induces apoptosis (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-10 family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AF276915; AAG16755.1; -; Genomic_DNA.
 CC EMBL; AF453946; AAN40906.1; -; mRNA.
 CC EMBL; AF192498; AAF06663.1; -; mRNA.
 CC EMBL; AY040367; AAK91776.1; ALT INIT; mRNA.
 CC EMBL; AP390905; AAK64498.1; -; Genomic_DNA.
 CC EMBL; AL049615; CAB72342.1; -; Genomic_DNA.
 CC PDB; 1INF; X-ray; A=19-177.
 CC Ensembl; ENSG00000142224; Homo sapiens.
 CC HGNC; HGNC:5990; IL19.
 CC MIM; 605687; -;
 CC GO; GO:0005576; C:extracellular region; NAS.
 CC GO; GO:0005125; F:cytokine activity; TAS.
 CC GO; GO:0006955; P:immune response; NAS.
 CC GO; GO:0007165; P:signal transduction; NAS.
 CC InterPro; IPR012351; Cytokine_4_hlx.
 CC InterPro; IPR000098; Interleukin_10.
 CC Pfam; PF00726; IL10; 1.
 CC SMART; SM00188; IL10; 1.
 CC PROSITE; PS00520; INTERLEUKIN_10; 1.
 CC 3D-structure; Apoptosis; Cytokine; Direct protein sequencing;
 KW Glycoprotein; Polymorphism; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 177 Interleukin-19.
 FT CARBOHYD 56 56 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 135 135 N-linked (GlcNAc...) (potential).
 FT DISULFID 28 121
 FT DISULFID 75 127
 FT DISULFID 76 129
 FT VARIANT 175 175 S->F.
 FT SEQUENCE 177 AA; 20392 MW; 7CCFAC22177DE408 CRC64;
 Query Match 37.1%; Score 337.5; DB 1; Length 177;
 Best Local Similarity 39.7%; Pred. No. 9.4e-25;
 Matches 69; Conservative 36; Mismatches 64; Indels 5; Gaps 1;
 QY 1 MKASIASFLSLAAFLYLTPTSTGKTLNLGSCVATNLOEIRNGFSIDRSGVQAKDGN 60
 DB 1 MKLQCVSLMLGLTILILCSVDNHLR-----RCLISTDMHHIBSFQEKALQAKDTPP 55

QY 61 DIRILARTESLOOTKPRANRCCLLRHLLRLYLDRVFNKYQTPDHVTLTKISLANSPLTIK 120
 DB 56 NVTILSTLETLQIKPLDVCCTVKNLAFYDVFVKDQEPNPKIRKISLANSFLYMQ 115
 QY 121 KDRLCHAHMTCGCEGEMKKYQSLSHPEKLEPOAAVVKALGELDILLQWME 174
 DB 116 KTLRQCGEORQCHGCEATNATNATVINDVQLEVHAALIKSGLDVLFLAMINK 169

RESULT 4
 OSVUT3 HUMAN
 ID OSVUT3 HUMAN PRELIMINARY; PRT; 215 AA.

DT 01-FEB-2005 (TEMBLrel. 29, Created)
 DT 01-FEB-2005 (TEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
 DE Interleukin 19.
 GN Name=IL19; ORFNames=RP11-262N9.2-001;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OC NCB1_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Kay M.;
 RC Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 DR EMBL; AL513115; CAH71814.1; -; Genomic DNA.
 DR SMR; OSVUT3; 60-215.
 DR Ensemble: ENSG00000142224; Homo sapiens.
 DR GO; GO:0005615; C:extracellular space; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN_10; UNKNOWN_1.
 KW Cytokine.
 KM
 SQ SEQUENCE 215 AA; 24567 MW; D79D6B0F1DA7AE4 CRC64;

Query Match 37.1%; Score 337.5; DB 2; Length 215;
 Best local Similarity 39.7%; Pred. No. 1.2e-24;
 Matches 69; Conservative 36; Mismatches 64; Indels 5; Gaps 1;

QY 1 MKASLSAFLSLAAYLLWTPSTGLTKLNLGSCVIATNQLRNGSDIRGVSQVADGNI 60
 DB 39 MKQCQSLMLLGLTILICSDVNHGLR-----RCILSTDMHIEESFQEI RRAIQADTFP 93
 QY 61 DIRILARTESLOOTKPRANRCCLLRHLLRLYLDRVFNKYQTPDHVTLTKISLANSPLTIK 120
 DB 94 NVTILSTLETLQIKPLDVCCTVKNLAFYDVFVKDQEPNPKIRKISLANSFLYMQ 153
 QY 121 KDRLCHAHMTCGCEGEMKKYQSLSHPEKLEPOAAVVKALGELDILLQWME 174
 DB 154 KTLRQCGEORQCHGCEATNATNATVINDVQLEVHAALIKSGLDVLFLAMINK 207

RESULT 5
 QALDR4 BRARE
 ID QALDR4 BRARE PRELIMINARY; PRT; 168 AA.
 AC QALDR4;
 DT 13-SEP-2005 (TEMBLrel. 31, Created)
 DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
 DE Interleukin 10 family protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCB1_TaxId=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ram S.; Datsuke I.; Sakai M.;

RT "Evolution of IL-10 family genes in teleosts."
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB219579; BAB06181.1; -; mRNA.
 SQ SEQUENCE 168 AA; 19110 MW; 807D18AD736C709B CRC64;

Query Match 33.6%; Score 306; DB 2; Length 168;
 Best local Similarity 42.4%; Pred. No. 1.1e-21;
 Matches 67; Conservative 27; Mismatches 58; Indels 6; Gaps 3;

QY 18 LWPSTGLTKLNLGSCVIATNQLRNGSDIRGVSQVADGNI DIRILR--TESLOOTK 75
 DB 10 LWDAAQG-RRLHIGSCVNIHTEHMHFQYRQGWISGDHKGIRLRDQVWSSLOAYE 68
 QY 76 PNRCCLLRHLLRLYLDRVFNKYQTPDHVTLTKISLANSPLTIK KDRLCHAHMTCG 135
 DB 69 ---SCCEFLQLHFYDVFISTSHSHRRRTSVLANSFISISKDLRCHAHMTCG 125
 QY 136 EEMKKYQSLSHPEKLEPOAAVVKALGELDILLQWME 173
 DB 126 ENTRQLKSIQRAYEKLDQAAGVAKALGELDSLIEWIE 163

RESULT 6
 IL19 MOUSE
 ID IL19 MOUSE STANDARD; PRT; 176 AA.
 AC O8CJ70;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-19 precursor (IL-19).
 GN Name=IL19;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCB1_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND FUNCTION.
 RC STRAIN=Swiss Webster / NIH;
 RX MEDLINE=42257669; PubMed=12370360;
 RT Liao Y.-C., Liang W.-G., Chen F.-W., Hsu J.-H., Yang J.-J., Chang M.-S.;
 RT "IL-19 induces production of IL-6 and TNF-alpha and results in cell
 RT apoptosis through TNF-alpha."
 RT J. Immunol. 169:4288-4297 (2002).
 CC -1- FUNCTION: May play some important roles in inflammatory responses.
 CC -1- UP-regulates IL-6 and TNF-alpha and induces apoptosis.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-10 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AF453945; AAN40905.1; -; mRNA.
 DR HSSP; Q9UHD0; INF.
 DR SMR; O8CJ70; 23-170.
 DR Ensemble; ENSMUSG0000016524; Mus musculus.
 DR MGI; MGI:1890472; IL19.
 DR GO; GO:0006917; P:induction of apoptosis; IDA.
 DR GO; GO:0042226; P:interleukin-6 biosynthesis; IDA.
 DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IDA.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000098; Interleukin_10.
 DR Prodom; PD003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN_10; FALSE NEG.
 KW Apoptosis; Cytokine; Glycoprotein; Signal.
 KW APOPTOSIS; CYTOKINE; GLYCOPROTEIN; SIGNAL.
 FT CHAIN 1 24 Potential.
 FT SIGNAL 25 176 Interleukin-19.
 FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).

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FT CARBOHYD 134 134 N-linked (GlcNAc...) (Potential).
FT DISUPID 28 120 By similarity.
FT DISUPID 74 126 By similarity.
FT DISUPID 75 128 By similarity.
SQ SEQUENCE 176 AA; 20288 MW; 73B6C1BC54077FDC CRC64;

Query Match
Best Local Similarity 30.9%; Score 281.5; DB 1; Length 176;
Matches 56; Conservative 33; Mismatches 53; Indels 1; Gaps 1;

QY 29 NLGSCVATNLQEIRNGFSDRGSVQAKGNIDIRILRTESLQDTKPNRCCILRLR 88
DB 24 SLRCLISVDMRIKSFHEIKRAMQTKQTFKAVTIL-SLENLRISIKRGDVCCTWNLTR 82
QY 89 LYLDRPKNYQTGDHNTLRKISSLANSFLTKDRLCHAHMTCHGSEAMKYSQLSL 148
DB 83 FYDRFVQDHSLEVLRISSINSLFCVOKSLERCQVHRQCNCSQETATNTRIHDN 142
QY 149 FEKLEPOAAVVKALGELDILLQWME 173
DB 143 YNLEVSAAKSLGELNILLAMID 167

RESULT 7
Q7SX60.TETNG
ID Q7SX60.TETNG PRELIMINARY; PRT; 175 AA.
AC Q7SX60;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Interleukin-20.
GN Name=IL20;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodon.
OX NCBI_Taxid=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12869211; DOI=10.1186/1471-2164-4-29;
RA Lutfalla G., Crolius H.R., Strange-Thomann N., Jallion O.,
Mogensen K., Monneron D.;
RT "Comparative genomic analysis reveals independent expansion of a
RT lineage-specific gene family in vertebrates: The class II cytokine
RT receptors and their ligands in mammals and fish.";
RL BMC Genomics 4:29-29(2003).
DR EMBL; AY294557; AAP57414.1; -; Genomic_DNA.
DR EMBL; AY294558; AAP57416.1; -; mRNA.
DR GO; GO:0005615; Extracellular space; IEA.
DR GO; GO:0005125; Fc cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
SQ SEQUENCE 175 AA; 19838 MW; DE6FA67E0038E034 CRC64;

Query Match
Best Local Similarity 29.3%; Score 266.5; DB 2; Length 175;
Matches 57; Conservative 33; Mismatches 53; Indels 7; Gaps 3;

QY 26 KTLNLGSCVATNLQEIRNGFSDRGSVQAKGNIDIRILRTESLQDTKPNRCCILRH 85
DB 24 OTLLVDSGISADLQEMHQHNSIRLNAITDEEIGVKLSK-RLMEDVDQDGRCCFLRL 82
QY 86 LRLYLDRPKNYQTGDHNTLRKISSLANSFLTKDRLCHAHMTCHGSEAMKYS 143
DB 83 VLQFYIDKVPFSLYSSHPQNSSSSLATFFIIVAKMIQKCH---CLCEQETQKQVD 138
QY 144 OILSHFEKLEPOAAVVKALGELDILLQWME 173

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DB 139 SLIDAFNKLEASKAVILKAVGELDTVLQWLQ 168

RESULT 8
Q925J3.MOUSE
ID Q925J3.MOUSE PRELIMINARY; PRT; 220 AA.
AC Q925J3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Th2-specific cytokine Flt3l.
GN Name=Il24;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX MEDLINE=21240641; PubMed=11342597;
RA Schaefer G., Venkataraman C., Schindler U.;
RT "Flt3l (Il-4-induced secreted protein), a novel cytokine-like molecule
RT secreted by Th2 cells.";
RL J. Immunol. 166:5859-5863(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; AF333251; AAK52470.1; -; mRNA.
DR Ensembl; ENSMUSG00000026420; Mus musculus.
DR MGI; MGI:2135548; Il24.
DR GO; GO:0005615; Extracellular space; TAS.
DR InterPro; IPR000098; Interleukin_10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KM Cytokine.
SQ SEQUENCE 220 AA; 25168 MW; 5BF6C8612AC090D CRC64;

Query Match
Best Local Similarity 24.4%; Score 222; DB 2; Length 220;
Matches 56; Conservative 30; Mismatches 71; Indels 6; Gaps 4;

QY 17 LMTPESTGL-KTLNLGSC-VIATNLQEIRNGFSDRGSVQAKGNIDIRILRTESLQD 73
DB 55 LLMNQVPGLEBQGFRRGSCQVTGVLPRLMEAFWTKNTVQDDITSIRLL-KPQVLRN 113
QY 74 TKPNRCCILRLRLYLDRPKNYQT--PDHYTLRKISSLANSFLTKDRLCHAHMT 131
DB 114 VSAESCVLAHSLKRYLNTVFNKYSKIAKFKVLRSFSTIANNFIVMSQLQPSKNSM 173
QY 132 CHGSEAMKYSQILSHFEKLEPOAAVVKALGELDILLQWME 174
DB 174 LPLISEAHORFLFRRAFKQDLTEVALVRAFGVDILLTMQK 216

RESULT 9
Q925S4.MOUSE
ID Q925S4.MOUSE PRELIMINARY; PRT; 181 AA.
AC Q925S4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Melanoma differentiation associated gene-7.
GN Name=Il24;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvJ;
RA Madiredi M.T., Lin J., Su Z., Shay J.W., Huberman B., Fisher P.B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBD databases.

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CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).

DR EMBL: AF235006; AKS2590.1; -, mRNA.

DR Ensembl: ENSMUSG0000026420; Mus musculus.

DR MGI: MGI:2153548; 1124.

DR GO: GO:0005615; Cytoplasmic space; TAS.

DR InterPro: IPR000098; Interleukin_10.

DR ProDom: PD003687; Interleukin_10; 1.

DR SMART: SM00188; IL10; 1.

DR PROSITE: PS00520; INTERLEUKIN_10; 1.

DR Cytokine.

SW SEQUENCE 181 AA; 20812 MW; 05CA43872D53555 CRC64;

Query Match 24.2%; Score 220; DB 2; Length 181;

Best Local Similarity 34.4%; Pred. No. 3.2e-13;

Matches 56; Conservative 30; Mismatches 71; Indels 6; Gaps 4;

QY 17 LWTPTSTGL--KTLNLGSC-VIATNLQEIINNGFSDIRGVSQVQAKDNIDIRLRRTSLQD 73

DB 16 LWNQVPGLEGQGFRRSSCGVTGVLPFLMEAFMTVNTVQTQDITSLRL-KPQVLRN 74

QY 74 TRPANRCCLRLRLRLYLDRVFNKYOT--PDHTLRKISLANSFLTIKQRLCHAMT 131

DB 75 VSGAESCYLAHSLDKFLKFLNTVFPKYSKIAKFKVLRSFSTLANNFIVMSQLPSPKNSM 134

QY 132 CHGGEAMKYSQILSHFEKLEPQAAVYKALGELDILQME 174

DB 135 LPISESHQRFLLFRRAFKQDTEVALVKAFGEVDILTMQK 177

RESULT 10

IL24_HUMAN STANDARD; PRT; 206 AA.

AC Q13007; Q96DB0; Q96KG4;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Interleukin-24 precursor (Suppression of tumorigenicity 16 protein)

DE (Melanoma differentiation-associated protein 7) (MDA-7).

OS Homo sapiens (Human).

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae;

OC Homo.

OX NCBI_TaxID=9606;

OC [1]

NC NUCLEOTIDE SEQUENCE.

RA Peat J., Kube D., Eskdale J., Jueliger S., Gallagher G.;

RC TISSUE=Melanoma;

RX MEDLINE=6132699; PubMed=8545104;

RA Jiang H., Lin J.J., Su Z.-Z., Goldstein N.I., Fisher P.B.;

RT "Subtraction hybridization identifies a novel melanoma differentiation associated gene, mda-7, modulated during human melanoma differentiation, growth and progression.";

RT Oncogene 11:2477-2486(1995).

RL [2]

NC NUCLEOTIDE SEQUENCE.

RA Peat J., Kube D., Eskdale J., Jueliger S., Gallagher G.;

RC "The human MDA-7 gene.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

NC NUCLEOTIDE SEQUENCE, AND VARIANT HIS-124.

RC TISSUE=Fibroblast;

RA Medireddi M.T., Lin J., Su Z.-Z., Shay J.W., Huberman E., Fisher P.B.;

RT "Genomic structure, chromosomal localization and expression of melanoma differentiation associated gene-7 (mda-7): potential relationship with cellular senescence.";

RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RL [4]

NC NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS HIS-124; ARG-125 AND LEU-131.

RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,

RA Peol C.L., Toth E.J., Yi O., Nickerson D.A.;

RT "SeattleSNP: NHLBI Hu6682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

[5]

NC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RP TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prence C.,

RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,

RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,

RA Schercher A., Schein J.E., Jones S.J.W., Maria M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[6]

RP PROTEIN SEQUENCE OF 52-66.

RX PubMed=15340161; DOI=10.1110/ps.04682504;

RA Zhang Z., Henzel W.J.;

RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites.";

RL Protein Sci. 13:2819-2824(2004).

[7]

NC CHARACTERIZATION.

RX MEDLINE=99045696; PubMed=9826712; DOI=10.1073/pnas.95.24.14400;

RA Su Z.-Z., Medireddi M.T., Lin J.J., Young C.S.H., Kitada S.,

RA Reed J.C., Goldstein N.I., Fisher P.B.;

RT "The cancer growth suppressor gene mda-7 selectively induces apoptosis in human breast cancer cells and inhibits tumor growth in nude mice.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:14400-14405(1998).

CC -1- FUNCTION: Has antiproliferative properties in human melanoma cells and may contribute to terminal cell differentiation. May also function as a negative regulator of melanoma progression.

CC Formation in vivo in nude mice. They found that it selectively induces apoptosis in human breast cancer cells.

CC -1- SUBCELLULAR LOCATION: Secreted (Potential).

CC -1- TISSUE SPECIFICITY: Up-regulated in melanoma cells induced to terminally differentiate.

CC -1- SIMILARITY: Belongs to the IL-10 family.

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CC -----

CC EMBL: U16261; AAA91780.1; -, mRNA.

CC EMBL: AF276916; AAG41401.1; -, Genomic DNA.

CC EMBL: AF235005; AKS2589.1; -, Genomic DNA.

CC EMBL: AY062931; AAL34146.1; -, Genomic DNA.

CC EMBL: BC009681; AAH09681.1; -, mRNA.

CC EMBL: ENSG00000162892; Homo sapiens.

CC HGN: HGNC:11346; IL24.

CC H-InvDB: HIX0001532; -.

CC MIM: 604136; -.

CC GO: GO:0006915; P:apoptosis; TAS.

CC InterPro: IPR012351; Cytokine_4_hlx.

CC InterPro: IPR000098; Interleukin_10.

CC ProDom: PD003687; Interleukin_10; 1.

CC SMART: SM00188; IL10; 1.

CC PROSITE: PS00520; INTERLEUKIN_10; 1.

CC Apoptosis; Cytokine; Direct protein sequencing; Glycoprotein;

CC Polymorphism; Signal.


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FT SIGNAL 1 51 Interleukin-24.
FT CHAIN 206 206 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 85 85 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 99 99 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 126 126 Y -> H (in dBSNP:1150258) .
FT VARIANT 124 124 /FTID=VAR 011974.
FT VARIANT 125 125 H -> R (in dBSNP:3093431) .
FT VARIANT 131 131 /FTID=VAR 013097.
FT VARIANT 131 131 V -> L (in dBSNP:3093446) .
FT CONFLICT 14 14 /FTID=VAR 013098.
FT CONFLICT 14 14 A -> AS (in Ref. 4) .
SQ SEQUENCE 206 AA; 23825 MW; CB8135083EAB8DD CRC64;

Query Match 23.8%; Score 217; DB 1; Length 206;
Best Local Similarity 32.8%; Pred. No. 7.3e-13;
Matches 57; Conservative 39; Mismatches 66; Indels 12; Gaps 5;

QY 6 LAFSLSAFYLLMTPTGL--KTLNAGSCVIATNL-OEIRNGPSDIRGSVOAKGNIDI 62
DB 36 LGFTL-----LLMSQVSGAGCGEHRFGCGVQKGVPOGLMEFAVAKDTMQADNITSA 89
QY 63 RLRTSTESLQDTKPNRCCLLRLHLRLYLDRVFKNY--QTPHYTLRKISLSANSEFLTIK 120
DB 90 RLLOQ-EVLQNVSDAESCYLVTHTLEFLYKTVFKYHNHTVEVRTLKSFTSLANNFVLIV 148
QY 121 KOLRLCHAMTCHGSEBANKKYSQILSHREKLEPQAAVVKALGELDILLQMMEE 174
DB 149 SOLQPSQENEMFSIRDSAHRRFLFRAPRKQDVEALTKALGEVDILLTMQK 202

RESULT 11
Q53XZ7 HUMAN PRELIMINARY; PRT; 207 AA.
ID Q53XZ7;
AC Q53XZ7;
DR 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Interleukin 24.
OS Homo sapiens (human) .
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Bisenstein S.,
RA Koudinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Pheilan M., Farmer A.;
RT "Cloning of human full-length cDNA in BD Creator(TM) System Donor
RT vector."
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; AB007156; AAP35820.1; -; mRNA.
DR GO; GO:0005576; Cytoplasmic region; IEA.
DR GO; GO:0005125; P:cytokine activity; IEA.
DR GO; GO:0006935; P:immune response; IEA.
DR Cytokine.
SQ SEQUENCE 207 AA; 23912 MW; 176874467B9CB551 CRC64;

Query Match 23.8%; Score 217; DB 2; Length 207;
Best Local Similarity 32.8%; Pred. No. 7.4e-13;
Matches 57; Conservative 39; Mismatches 66; Indels 12; Gaps 5;
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DB 150 SOLQPSQENEMFSIRDSAHRRFLFRAPRKQDVEALTKALGEVDILLTMQK 203

RESULT 12
MOBS RAT
ID MOBS RAT STANDARD; PRT; 183 AA.
AC 09J174;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cytokine-like protein Mob-5 precursor.
GN Name=MOBS;
OS Rattus norvegicus (Rat) .
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20387329; PubMed=10825166; DOI=10.1074/jbc.M001958200;
RA Zhang R., Tan Z., Liang P.;
RT "Identification of a novel ligand-receptor pair constitutively
RT activated by ras oncogenes."
RL J. Biol. Chem. 275:24436-24443(2000) .
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-10 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF269251; AAF7553.1; -; mRNA.
DR Ensembl; ENSRN00000004470; Rattus norvegicus.
DR GO; GO:0048144; P:fibroblast proliferation; TAS.
DR GO; GO:0042060; P:wound healing; TAS.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR000098; Interleukin_10.
DR ProDom; PD003687; Interleukin_10.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KM Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 183 Cytokine-like protein Mob-5.
FT CARBOHYD 76 76 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 183 AA; 21096 MW; AF7A11466C491AC4 CRC64;

Query Match 21.0%; Score 191; DB 1; Length 183;
Best Local Similarity 33.1%; Pred. No. 2.2e-10;
Matches 49; Conservative 31; Mismatches 60; Indels 8; Gaps 5;

QY 31 GSC-VIATNLQIRNGPSDIRGSVOAKGNIDIRILRRESLODTKPNRCCLLRLHL 89
DB 34 GPCQYTGVLPLMEAFWTKVTKYQDELTSVRL-KQVLQNVSDASCTLSANSLKLF 92
QY 90 YLDRVFKNYQTP--DHYTLRKISLSANSEFLTIKQDLRCHAMTCHGSEBANKKYSQILS 147
DB 93 YLNTVFKNVKHSKIYKFKVLKSPSTLANNFLVIMSKLQPSKDAMLPISDSARRF--LLY 150
QY 148 H--FEKLEPQAAVVKALGELDILLQMMEE 173
DB 151 HRTFKQLDIEVALAKAFGEVDILLAMQ 178

RESULT 13
Q9WVP8 RAT PRELIMINARY; PRT; 183 AA.
ID Q9WVP8;
AC Q9WVP8;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
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DE C49a.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=99308986; PubMed=10381256;
RX DOI=10.1002/(SICI)1097-4644(1990701)74:1<1::AID-JCB1>3.3.CO;2-D;
RA Seo C., Shaw W.W., Freymiller E., Longaker M.T., Bertolami C.N.,
RA Chiu R., Tieu A., Ting K.;
RT "Cutaneous rat wounds express c49a, a novel gene with homology to the
RT human melanoma differentiation associated gene, mda-7."
RL J. Cell. Biochem. 74:1-10(1999).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC EMBL: AF004774; AAB69171.1; -; mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR000098; Interleukin_10.
DR ProDom: PD003687; Interleukin_10.
DR PROSITE: PS00520; INTERLEUKIN_10; 1.
KW Cytokine.
SQ SEQUENCE 183 AA; 21052 MW; FF69A96AFC473E4F CRC64;

Query Match 20.5%; Score 187; DB 2; Length 183;
Best Local Similarity 32.2%; Pred. No. 5.5e-10;
Matches 47; Conservative 29; Mismatches 66; Indels 4; Gaps 3;

QY 31 GSC-VIATNIOEIRNGSFDIRGVSQAKDNIDIRLRISLDPTKPNACCLRLHLR 89
DB 34 GPCQVGVVPELMEAPWTKVTKYDDELTSARLL-KPVLQNVSDAESCYLAHSILK 92
QY 90 YLDKVFKNYQTP--DHYTLKRISLANSFLTIKKDLRLCHAMTCHGCEBAMKKYSQILS 147
DB 93 YLNVTFKNYSKYVKRVKLVKSPSTLANPFLVMSKQPSKDNMLPISDARRRFLFLFR 152
QY 148 HFEKLEPQAAVKAAGELDILLQWME 173
DB 153 TFKQLDIEVALAKAFGEVDILLAMQ 178

RESULT 14
ID 06A2H5 CHICK PRELIMINARY; PRT; 175 AA.
AC 06A2H5;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Interleukin-10.
GN Name=IL-10;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rothwell L., Young J., Zoorob R., Whitaker C.A., Heeketh P.,
RA Archer A., Smith A.L., Kaiser P.;
RT "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT Immune Response to Eimeria maxima."
RL J. Immunol. 173:2675-2682(2004).
CC EMBL: AJ621254; CAF18432.1; -; mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR012351; Cytokine_4_hlx.
DR InterPro: IPR012352; IL-10 add helix.
DR InterPro: IPR000098; Interleukin_10.
DR Pfam: PF00726; IL10; 1.

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DR PRINTS: PR01294; INTERLEUKIN10.
DR ProDom: PD003687; Interleukin_10; 1.
DR SMART: SM00188; IL10; 1.
SQ SEQUENCE 175 AA; 20514 MW; B0966BEBADF050 CRC64;

Query Match 19.3%; Score 175.5; DB 2; Length 175;
Best Local Similarity 30.3%; Pred. No. 7e-09;
Matches 53; Conservative 32; Mismatches 81; Indels 9; Gaps 5;

QY 1 MKASSLAFSLNAPFLWTPSTGLKTLNIG-SCVIATNLQEIIRNGFSDIRGSVQAKDN 59
DB 1 MGTCCQALLILLAACTL---PAHCLEPTCLHSEBLPARLRKRVAFEEIKDYQSRDDE 57
QY 60 IDIRILRTESLDPTKPNARCCILRLRLYLDRVFNKVTQDPHYTLRKISSLANSFLTI 119
DB 58 LNIQLL-SSLDLDFGTGCGSVSEMLRFTDEVLPAMQSTSHQSGMDIGNMLGL 116
QY 120 KDLRLCHAMTCHGCEBAMKKYSQILSHFEKLEPQAAVKAAGELDILLQWME 174
DB 117 KATMRCHRFPTC---EKSKAIKQIKETFEKMD-ENGIIKAMGEFDIFNTYIE 167

RESULT 15
ID 06A2H4 CHICK PRELIMINARY; PRT; 175 AA.
AC 06A2H4;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Interleukin-10.
GN Name=IL10;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rothwell L., Young J., Zoorob R., Whitaker C.A., Heeketh P.,
RA Archer A., Smith A.L., Kaiser P.;
RT "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT Immune Response to Eimeria maxima."
RL J. Immunol. 173:2675-2682(2004).
CC EMBL: AJ621254; CAF21727.1; -; Genomic DNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR012351; Cytokine_4_hlx.
DR InterPro: IPR012352; IL-10 add helix.
DR InterPro: IPR000098; Interleukin_10.
DR Pfam: PF00726; IL10; 1.
DR PRINTS: PR01294; INTERLEUKIN10.
DR ProDom: PD003687; Interleukin_10; 1.
DR SMART: SM00188; IL10; 1.
SQ SEQUENCE 175 AA; 20496 MW; A4966ABAAPFB057 CRC64;

Query Match 19.3%; Score 175.5; DB 2; Length 175;
Best Local Similarity 30.3%; Pred. No. 7e-09;
Matches 53; Conservative 32; Mismatches 81; Indels 9; Gaps 5;

QY 1 MKASSLAFSLNAPFLWTPSTGLKTLNIG-SCVIATNLQEIIRNGFSDIRGSVQAKDN 59
DB 1 MGTCCQALLILLAACTL---PAHCLEPTCLHSEBLPARLRKRVAFEEIKDYQSRDDE 57
QY 60 IDIRILRTESLDPTKPNARCCILRLRLYLDRVFNKVTQDPHYTLRKISSLANSFLTI 119
DB 58 LNIQLL-SSLDLDFGTGCGSVSEMLRFTDEVLPAMQSTSHQSGMDIGNMLGL 116
QY 120 KDLRLCHAMTCHGCEBAMKKYSQILSHFEKLEPQAAVKAAGELDILLQWME 174
DB 117 KATMRCHRFPTC---EKSKAIKQIKETFEKMD-ENGIIKAMGEFDIFNTYIE 167

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Search completed: December 24, 2005, 10:31:59
Job time : 230 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: December 28, 2005, 11:43:57 / Search time 2945 Seconds
(without alignments)
2779.442 Million cell updates/sec

Title: US-10-789-251-26
Perfect score: 753
Sequence: 1 CVIATNLOEIRNGFSDIRG.....AVKALGHELDILLQWMEETE 144

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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15: gb_pl:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	753	100.0	926	BD087297 Mammalian
2	753	100.0	926	CO818183 Sequence
3	753	100.0	926	CS109174 Sequence

Result No.	Score	Query Match Length	ID	Description
4	753	100.0	926	CS110179 Sequence
5	753	100.0	926	AR342856 Sequence
6	753	100.0	926	AF224266 Homo sapi
7	749	99.5	462	CS123418 Sequence
8	749	99.5	531	BC069311 Homo sapi
9	749	99.5	531	BC069364 Homo sapi
10	749	99.5	531	BC069398 Homo sapi
11	749	99.5	531	BC069425 Homo sapi
12	749	99.5	531	BC069449 Homo sapi
13	749	99.5	531	BC069487 Homo sapi
14	749	99.5	531	BC069523 Homo sapi
15	749	99.5	531	BC069559 Homo sapi
16	749	99.5	531	AY888562 Synthetic
17	749	99.5	531	AY891211 Synthetic
18	749	99.5	531	AY893295 Synthetic
19	749	99.5	603	BC074948 Homo sapi
20	749	99.5	603	BC074949 Homo sapi
21	749	99.5	867	AX498605 Sequence
22	749	99.5	867	AX537938 Sequence
23	746	99.1	926	CO889881 Sequence
24	746	99.1	926	CO889943 Sequence
25	739	98.1	1571	CQ970652 Sequence
26	739	98.1	1571	CS133455 Sequence
27	739	98.1	1571	AX092406 Sequence
28	739	98.1	1571	AX358964 Sequence
29	739	98.1	1571	AX362457 Sequence
30	739	98.1	1571	AX376542 Sequence
31	739	98.1	1571	AX454700 Sequence
32	739	98.1	1571	AX463964 Sequence
33	739	98.1	1571	AX464412 Sequence
34	739	98.1	1571	AX491178 Sequence
35	739	98.1	1571	AX697333 Sequence
36	739	98.1	1571	AY358320 Homo sapi
37	686	91.1	747	BD087304 Mammalian
38	686	91.1	747	CO818192 Sequence
39	686	91.1	747	CS109203 Sequence
40	686	91.1	747	CS110208 Sequence
41	686	91.1	747	AR342863 Sequence
42	587.5	78.0	793	BD087298 Mammalian
43	587.5	78.0	793	CO818185 Sequence
44	587.5	78.0	793	CS109177 Sequence
45	587.5	78.0	793	CS110182 Sequence

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
Mammalian cytokine-like polypeptide-10.
ACCESSION
BD087297.1 GI:22632907
VERSION
JP 2001524313-A/1.
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 926)
Conklin,D.C., Haldeman,B.A. and Grossmann,A.
Mammalian cytokine-like polypeptide-10
Patent: JP 2001524313-A 1 04-DEC-2001;
ZymoGenetics INC
OS
Homo sapiens (human)
PN
JP 2001524313-A/1
PD
04-DEC-2001
PF
25-NOV-1998 JP 2000522245
PR
26-NOV-1997 US 08/979156
PI
DARRELL C CONKLIN, BETTY A HALDEMAN, ANGELIKA GROSSMANN PC
C12N15/09, A01K67/027, A61K38/00, A61K48/00, A61P1/02, A61P11/00, PC
A61P17/00,
PC
A61P35/00, A61P37/02, A61P43/00, C07K14/52, C07K16/24, C07K16/42, PC
C12N15/00,

PC A61K37/02
CC Mammalian cytokine-like polypeptide-10
FT Key Location/Qualifiers
CDS (45) . (572) .

FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

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Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-789-251-26 (1-144) x BD087297 (1-926)

QY 1 CysValIleAlaThrAsnLeuGlnIuIleArgAsnGlyPheSerAspIleArgGlySer 20
141 TGGTGATCGCCCAAACTTCAGAAATAGAAATGATTTCTGACATACGGGGCAGT 200
QY 21 ValGlnAlaIysAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
201 GTGCAGACCAAAAGTGAACATTTGACATCAGATCTTAAGAGAGACTGAGTCTTGCAA 260
QY 41 AspThrIysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrlLeuAsp 60
261 GACCAAAAGCTCGAAATCGATGCTGCTCCTCGGCCATTTGCTAAAGCTCTATCTGGAC 320
QY 61 ArgValPheIysAsnTyrlGlnThrProAspHisTyrlThrLeuArgIlysIleSerSerLeu 80
321 AGGTTATTTAAACCTACAGAGACCCCTGACCATTAATCTCCGGAAGATCAGAGCCTC 380
QY 81 AlaAsnSerPheLeuThrIleIysIysAspLeuArgLeuCysHisAlaHisMetThrCys 100
381 GCCAATTCCTTTCTTACCATCAAGAAAGACCTCGGCTCTGTCTATGCCCATGACATGC 440
QY 101 HisCysGlyGlnIuIuAlaMetIysIysTyrlSerGlnIleLeuSerHisPheGlnIysLeu 120
441 CATTGGGGAGAGCAATGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500
QY 121 GluProGlnAlaAlaValIysAlaLeuGlyGlnLeuAspIleLeuLeuGlnTrpMet 140
501 GAACCTCAGGCAGCAGTTGTGAAGCTTTGGGGAACTAGACATTTCTTGCATGTGATG 560
QY 141 GluGlnThrGln 144
561 GAGAGACAGAA 572

RESULT 2
CQ0818183
LOCUS CQ0818183 926 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 1 from Patent EP1424393.
ACCESSION CQ0818183
VERSION CQ0818183.1 GI:48426975
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS Conklin,D.C., Haldeman,B.A. and Grossmann,A.
TITLE Mammalian cytokine-like polypeptide-10
JOURNAL Patent: EP 1424393-A 1 02-JUN-2004;
Zymogenetics Inc (US)
FEATURES
source 1..926
/organism="Homo sapiens"

CDS
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
45..575
/note="unnamed protein product"
/codon_start=1
/protein_id="CAG33976.1"
/db_xref="GI:48426976"
/translation="MKASSLAFSLISAAYLLMTPESTGLKTLNLSGCVIATNLQEI RN
GSDIDGVSQAKDGNIDIRILRRTESLQOTKPRNRCCILRHLLRLVDYFKYQTPD
HYLRKISLSANSLITTKDRLRCHAHMTCHGEEAMKKYSQTLSPFEKLEPOAAVVK
ALGEIDILLQWMEETE"

ORIGIN

Alignment Scores:
Pred. No.: 3,22e-72 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-789-251-26 (1-144) x CQ0818183 (1-926)

QY 1 CysValIleAlaThrAsnLeuGlnIuIleArgAsnGlyPheSerAspIleArgGlySer 20
141 TGGTGATCGCCCAAACTTCAGAAATAGAAATGATTTCTGACATACGGGGCAGT 200
QY 21 ValGlnAlaIysAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
201 GTGCAGACCAAAAGTGAACATTTGACATCAGATCTTAAGAGAGACTGAGTCTTGCAA 260
QY 41 AspThrIysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrlLeuAsp 60
261 GACCAAAAGCTCGAAATCGATGCTGCTCCTCGGCCATTTGCTAAAGCTCTATCTGGAC 320
QY 61 ArgValPheIysAsnTyrlGlnThrProAspHisTyrlThrLeuArgIlysIleSerSerLeu 80
321 AGGTTATTTAAACCTACAGAGACCCCTGACCATTAATCTCCGGAAGATCAGAGCCTC 380
QY 81 AlaAsnSerPheLeuThrIleIysIysAspLeuArgLeuCysHisAlaHisMetThrCys 100
381 GCCAATTCCTTTCTTACCATCAAGAAAGACCTCGGCTCTGTATGCCCATGACATGC 440
QY 101 HisCysGlyGlnIuIuAlaMetIysIysTyrlSerGlnIleLeuSerHisPheGlnIysLeu 120
441 CATTGGGGAGAGCAATGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500
QY 121 GluProGlnAlaAlaValIysAlaLeuGlyGlnLeuAspIleLeuLeuGlnTrpMet 140
501 GAACCTCAGGCAGCAGTTGTGAAGCTTTGGGGAACTAGACATTTCTTGCATGTGATG 560
QY 141 GluGlnThrGln 144
561 GAGAGACAGAA 572

RESULT 3
CS109174
LOCUS CS109174 926 bp DNA linear PAT 22-JUN-2005
DEFINITION Sequence 1 from Patent WO2005052001.
ACCESSION CS109174
VERSION CS109174.1 GI:68148023
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS Xu,W., Kindvogel,W.R., Chen,Z., Hughes,S.D., Chandrasekhar,Y.A.,
Dillon,S.R., Lehnert,J.M., Sladek,A.W., Sivakumar,P.V. and
Moore,M.D.
TITLE Anti-IL-20 receptor antibodies and binding partners and methods of
using in inflammation

JOURNAL Patent: WO 2005052000-A 1 09-JUN-2005;
ZymoGenetics, Inc. (US)
FEATURES Location/Qualifiers
source 1..926
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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CDS
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/db_xref="GI:68148024"
/translation="MKASSLAFSLNSAFYLTWPSTGLTKTLNLSGVATNLQELRN
GFSDIRGSVOAKDGNIDIRLRRTESLDPTKPNRCCILRLRLYLDRVFKYOTPD
HTLRKISSLSANFLTIKDKDLRLCHAHMTCHGSEEMKKYSQILSHPEKLEPQAAVVK
ALGELDILQNMHEETE"

ORIGIN

Alignment Scores:

Pred. No.: 3,22e-72 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-789-251-26 (1-144) x CS109174 (1-926)

QY 1 CysValIleAlaThrAnLeuGInGluIleArgAsnGlyPheSerApIleArgGlySer 20
Db 141 TGTGTATCGCCCAAACTTCAGAAATACGAAATGATTTTCTGACATACGGGCGAGT 200
QY 21 ValGlnAlaIleAspArgIleAspIleArgIleLeuArgArgThrGlySerLeuGln 40
Db 201 GTGCACCAAGCCCAAGATGAAACATTGACATGAGATCTTAAGAGAGACTGAGTCTTGCAA 260
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrlLeuAsp 60
Db 261 GACACAAAGCCTCGAATGATGATGCTGCTCTCGCCATTGGCTAAGACTCTATCTGGAC 320
QY 61 ArgValPheIleAsnTyrlGlnThrProAspHisTyrlThrLeuArgIleSerSerLeu 80
Db 321 AGGGTATTTAAAACATACAGACCCCTGACCATTAATCTCTCGGAAAGATCAGACGCTC 380
QY 81 AlaAsnSerPheLeuThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100
Db 381 GCCAATTCCTTCTTACCATCAAGAGAGACCTCGGCTGTGATGCCCCATGACATGCG 440
QY 101 HisCysGlyGlyGlnAlaMetIleIleIleIleIleIleIleIleIleIleIleIleIleIle 120
Db 441 CATTGTGGGAGAGACATGAAATACAGCCAGATTCGAGTCACTTGAAGAGCTG 500
QY 121 GlnProGlnAlaIleValIleValIleValIleValIleValIleValIleValIleValIle 140
Db 501 GAACCTCAGGACAGCATGTGTGAAGGCTTTGGGGAACTAGACATTTCTTCGACATGATG 560
QY 141 GlnGlnThrGln 144
Db 561 GAGGAGACAGAA 572

RESULT 4
LOCUS CS110179 926 bp DNA linear PAT 22-JUN-2005
DEFINITION Sequence 1 from Patent WO2005052000.
ACCESSION CS110179
VERSION CS110179.1 GI:68148437
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1

AUTHORS Xu, W., Kindsvogel, W.R., Chen, Z., Hughes, S.D., Chandrasekhar, Y.A.,
Dillon, S.R., Lehner, J.M., Siadek, A.W., Sivakumar, P.V. and
Moore, M.D.
TITLE Anti-IL-12 antibodies and binding partners and methods of using in
inflammation
JOURNAL Patent: WO 2005052000-A 1 09-JUN-2005;
ZymoGenetics, Inc. (US)
FEATURES Location/Qualifiers
source 1..926
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
45..575
CDS
/note="unnamed protein product"
/codon_start=1
/protein_id="CAJ09906.1"
/db_xref="GI:68148438"
/translation="MKASSLAFSLNSAFYLTWPSTGLTKTLNLSGVATNLQELRN
GFSDIRGSVOAKDGNIDIRLRRTESLDPTKPNRCCILRLRLYLDRVFKYOTPD
HTLRKISSLSANFLTIKDKDLRLCHAHMTCHGSEEMKKYSQILSHPEKLEPQAAVVK
ALGELDILQNMHEETE"

ORIGIN

Alignment Scores:

Pred. No.: 3,22e-72 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-789-251-26 (1-144) x CS110179 (1-926)

QY 1 CysValIleAlaThrAnLeuGInGluIleArgAsnGlyPheSerApIleArgGlySer 20
Db 141 TGTGTATCGCCCAAACTTCAGAAATACGAAATGATTTTCTGACATACGGGCGAGT 200
QY 21 ValGlnAlaIleAspArgIleAspIleArgIleLeuArgArgThrGlySerLeuGln 40
Db 201 GTGCACCAAGCCCAAGATGAAACATTGACATGAGATCTTAAGAGAGACTGAGTCTTGCAA 260
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrlLeuAsp 60
Db 261 GACACAAAGCCTCGAATGATGATGCTGCTCTCGCCATTGGCTAAGACTCTATCTGGAC 320
QY 61 ArgValPheIleAsnTyrlGlnThrProAspHisTyrlThrLeuArgIleSerSerLeu 80
Db 321 AGGGTATTTAAAACATACAGACCCCTGACCATTAATCTCTCGGAAAGATCAGACGCTC 380
QY 81 AlaAsnSerPheLeuThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100
Db 381 GCCAATTCCTTCTTACCATCAAGAGAGACCTCGGCTGTGATGCCCCATGACATGCG 440
QY 101 HisCysGlyGlyGlnAlaMetIleIleIleIleIleIleIleIleIleIleIleIleIleIle 120
Db 441 CATTGTGGGAGAGACATGAAATACAGCCAGATTCGAGTCACTTGAAGAGCTG 500
QY 121 GlnProGlnAlaIleValIleValIleValIleValIleValIleValIleValIleValIle 140
Db 501 GAACCTCAGGACAGCATGTGTGAAGGCTTTGGGGAACTAGACATTTCTTCGACATGATG 560
QY 141 GlnGlnThrGln 144
Db 561 GAGGAGACAGAA 572

RESULT 5
LOCUS AR342856 926 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6576743.
ACCESSION AR342856
VERSION AR342856.1 GI:33738131
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 926)
AUTHORS Konklin,D.C. and Haldeman,B.A.
TITLE Mammalian cytokine-like polypeptide-10
JOURNAL Patent: US 6576743-A 1 10-JUN-2003;
ZymoGenetics, Inc.; Seattle, WA
FEATURES
Source Location/Qualifiers
1..926
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 3,22e-72 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6
US-10-789-251-26 (1-144) x AR32856 (1-926)
QY 1 CyeValIleAlaThrAsnLeuGlnIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 141 TGTGTGATCGCCCAAACTTCAGAAATACGAAATGATTTTCTGACATACGGGGCAGT 200
QY 21 ValGlnAlaIlyAspArgIlyAsnIleAspIleArgIleLeuArgArgThrGln 40
DB 201 GTGCAGCCCAAGATGGAACATTGACATCAGATCTTAAGAGAGACTGAGTCTTTGCCA 260
QY 41 AspThrIlySerProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuIlyLeuAsp 60
DB 261 GACACAAAGCGCTGGATGATGATGCTGCTGCTGCGCAATTTGCTAAGACTCTATCTGGAC 320
QY 61 ArgValIleAlaThrAsnLeuGlnIleProAspHisIleThrLeuArgIlyIleSerSerLeu 80
DB 321 AGGTTATTTTAAATCTACAGACCCCTGACCATTTATCTCTCGGAAGATCAGACGCTC 380
QY 81 AlaAsnSerPheLeuThrIleIlyIlyIlyAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 381 GCCAATTCCTTTCTTACATCAAGAGAGACCTCGGCTGTGTATGCTCCACATGACATGC 440
QY 101 HisCysGlyGlnGlnAlaMetIlyIlyIlyIlySerGlnIleLeuSerHisPheGlnIlyLeu 120
DB 441 CATTTGGGGAGAGCAATGAGAAATACAGCCAGATTTCTGACTCATTTGAAAGACTG 500
QY 121 GluProGlnAlaIlyValIlyValIleAlaLeuGlnIlyIlyLeuAspIleLeuLeuGlnTrpMet 140
DB 501 GAACCTCAGCGACAGATTTGTGAGGCTTTGGGGAGACTAGACATTTCTTGTGCATGGAGT 560
QY 141 GluGlnIlyThrGln 144
DB 561 GAGGAGACAGAA 572
RESULT 6
AF224266 926 bp mRNA linear PRI 24-JAN-2001
LOCUS Homo sapiens four alpha helix cytokine (ZCYTO10) mRNA, ZCYTO10-1
DEFINITION AF224266
AF224266 complete cds.
VERSION AF224266.1 GI:7109206
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 926)
AUTHORS Konklin,D., Xu,W.F., Grossmann,A., Brendler,T.,
Blumroth,S., Bagan,M., Foster,D., Haldeman,B.A., Hammond,A.,
Haugen,H., Jelinek,L., Kelly,J.D., Madden,K., Maurer,M.F.,
Parish-Novak,J., Prunkard,D., Sexson,S., Sprecher,C., Waggle,K.,
West,J., Whitmore,T.E., Yao,L., Kuechle,M.K., Dale,B.A. and
Chandrasekhar,V.A.
Interleukin 20: discovery, receptor identification, and role in
epidermal function
Cell 104 (1), 9-19 (2001)
11163236
JOURNAL PUBMED
2 (bases 1 to 926)
AUTHORS Konklin,D., Grossmann,A., Haldeman,B. and O'Hara,P.
TITLE Homo sapiens four alpha helix cytokine allele 1
REFERENCE 3 (bases 1 to 926)
JOURNAL Unpublished
AUTHORS Konklin,D., Grossmann,A., Haldeman,B. and O'Hara,P.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2000) Biomedical Informatics, ZymoGenetics,
Inc., 1201 Baerlake Ave. East, Seattle, Wa. 98102, USA
FEATURES
Source Location/Qualifiers
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/mol_type="mRNA"
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/map="1q32.2"
1..926
/gene="ZCYTO10"
/allele="1"
/codon_start=1
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/protein_id="AAF36679.1"
/db_xref="GI:7109207"
/translation="MKASLAFSLISAAYILMTPTSGTKTLNLSGVIALTNLQELRN
GFSIDRGSYQAKDGNIDIRILRTBSLDQTKRANRCLRHILRLYLIDVRFKRYQTPD
HTLRLKISLANSPLTKDRLRCHAHMTCGSEAMKYSQILSHFEKLEPQAAVVK
ALGELDILQWMBETE"

ORIGIN
Alignment Scores:
Pred. No.: 3,22e-72 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 8
US-10-789-251-26 (1-144) x AF224266 (1-926)
QY 1 CyeValIleAlaThrAsnLeuGlnIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 141 TGTGTGATCGCCCAAACTTCAGAAATACGAAATGATTTTCTGACATACGGGGCAGT 200
QY 21 ValGlnAlaIlyAspArgIlyAsnIleAspIleArgIleLeuArgArgThrGln 40
DB 201 GTGCAGCCCAAGATGGAACATTGACATCAGATCTTAAGAGAGACTGAGTCTTTGCCA 260
QY 41 AspThrIlySerProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuIlyLeuAsp 60
DB 261 GACACAAAGCGCTGGATGATGATGCTGCTGCTGCGCAATTTGCTAAGACTCTATCTGGAC 320
QY 61 ArgValIleAlaThrAsnLeuGlnIleProAspHisIleThrLeuArgIlyIleSerSerLeu 80
DB 321 AGGTTATTTTAAATCTACAGACCCCTGACCATTTATCTCTCGGAAGATCAGACGCTC 380
QY 81 AlaAsnSerPheLeuThrIleIlyIlyIlyAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 381 GCCAATTCCTTTCTTACATCAAGAGAGACCTCGGCTGTGTATGCTCCACATGACATGC 440
QY 101 HisCysGlyGlnGlnAlaMetIlyIlyIlyIlySerGlnIleLeuSerHisPheGlnIlyLeu 120
DB 441 CATTTGGGGAGAGCAATGAGAAATACAGCCAGATTTCTGACTCATTTGAAAGACTG 500
QY 121 GluProGlnAlaIlyValIlyValIleAlaLeuGlnIlyIlyLeuAspIleLeuLeuGlnTrpMet 140

Db	501	GAACTTACGACGAGCTTGGAGGCTTTGGGGAACTAGACATTCTTCTGCAATGATG	560
Qy	141	GIUGlUthrglu 144	
Db	561	GAGGAGACAGAA 572	
RESULT 7			
LOCUS	CS123418	462 bp	DNA
DEFINITION	Sequence 18 from Patent WO2005058946.		linear
ACCESSION	CS123418		PAT 16-JUL-2005
VERSION	CS123418.1	GI:70911957	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Chan, C.		
TITLE	Methods for enhancing expression of recombinant proteins		
JOURNAL	Patent: WO 2005058946-A 18 30-JUN-2005;		
FEATURES			
source			
ORIGIN			
Alignment Scores:			
Pred. No.:	4,066-72	Length:	462
Score:	749.00	Matches:	143
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.31%	Mismatch:	0
Query Match:	99.47%	Indels:	0
DB:	6	Gaps:	0
US-10-789-251-26 (1-144) x CS123418 (1-462)			
Qy	1	Cyevalllealathraenleuglnlilearghnglypheserapllearglyser	20
Db	28	TGTGTATCCCAACCACTGACGGAATCCGTAACTCTCTGAGATCCGTCGACG	87
Qy	21	ValGlnAlalyaapglYaenlleapllearglleleuargargthrgluserleuGln	40
Db	88	GTCGAGGCCAAAGTGTAACTTGAATCCGTATCTGCGTACCGAGTCTTCGACG	147
Qy	41	AspThrlyAspProAlaAnaArgCyseleuLeuArgHlsleuLeuArgLeuArgYrleuAsp	60
Db	148	GACACCAACCGCGAACCTGTGCTGCTGCGCACTGCTGCTGCTGCTGCTGCTGCTG	207
Qy	61	ArgValPheleYsaenYrGlnThrProAspHlsYrThrleuArglylseserleu	80
Db	208	CGTGTTCCTTCAAAATCAACAGACCCCGACCACTATACCTGCGTAAATCAGACGCTG	267
Qy	81	AlaAsnSerPheleuThrllelylybAspleuArgleuCyshAlaAlaSmethrCyse	100
Db	268	GCCAACTCTTCTGACCATCAAAAGACCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGT	327
Qy	101	HlsCGeGlygluGlualameClylybYrSerGlnlleuserHlsPheGlylybYrleu	120
Db	328	CACCTGT	387
Qy	121	GluPrgGlnAlaAlaValVallybAlaLeuGlygluLeuAspilleuLeuGlnTrpMet	140
Db	388	GAAACCGAGGACAGAGTGTGAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	447
Qy	141	GIUGlUthrglu 144	
Db	448	GAGGAGACCGAA 459	
RESULT 8			
BC069311			
LOCUS	BC069311	531 bp	mRNA
DEFINITION	Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96907		linear
ACCESSION	BC069311		PRI 06-JUL-2005
VERSION	BC069311.1	GI:47480994	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS			
STRAUSSBERG, R.L., FEINGOLD, E.A., GROUSE, L.H., DERGE, J.G.,			
KLAUSNER, R.D., COLLINS, F.S., WAGNER, L., SHENMEN, C.M., SCHULER, G.D.,			
ALTSCHUL, S.F., ZEEBERG, B., BUELOW, K.H., SCHAEFER, C.F., BHAC, N.K.,			
HOPKINS, R.F., JORDAN, H., MOORE, T., MAX, S.T., WANG, J., HALE, F.,			
DATCHENKO, L., MARUSINA, K., FARMER, A.A., RUBIN, G.M., HONG, L.,			
SCAPLETON, M., SOARES, M.B., BONALDO, M.F., CASAVANT, T.L.,			
SCHAEFER, T.E., BROWNSTEIN, M.J., USLIN, T.B., TOCHIYUKI, S.,			
CARNINCI, P., PRANGE, C., RAHA, S.S., LOQUELLANO, N.A., PETERS, G.J.,			
ABRAMSON, R.D., MULIANY, S.J., BOSAK, S.A., MCEWAN, F.J.,			
MCKERNAN, K.J., HALE, S., GARCIA, A.M., GAY, L.J., HULYK, S.W.,			
WORTLEY, K.C., HALE, S., GARCIA, A.M., GAY, L.J., HULYK, S.W.,			
VILLALON, D.K., MUZNY, D.M., SODERGREN, E.J., LU, X., GIBBS, R.A.,			
FANEY, J., HELTON, E., KETEMAN, M., MADAN, A., RODRIGUES, S.,			
SANCHEZ, A., WHITING, M., MADAN, A., YOUNG, A.C., SHIVCHENKO, Y.,			
BOUFFARD, G.G., BLAKESLEY, R.W., TOUCHMAN, J.W., GREEN, E.D.,			
DICKSON, M.C., RODRIGUEZ, A.C., GRIMWOOD, J., SCHMUTZ, J., MYERS, R.M.,			
BUTTERFIELD, Y.S., KRZYWINSKI, M.I., SKALSKA, U., SNAIUS, D.E.,			
SCHNERCH, A., SCHEIN, J.E., JONES, S.J. and MARRA, M.A.			
Mammalian Gene Collection Program Team			
Generation and initial analysis of more than 15,000 full-length			
human and mouse cDNA sequences			
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
12477932			
2 (bases 1 to 531)			
NIH MGC Project			
Direct Submission			
Submitted (29-APR-2004) National Institutes of Health, Mammalian			
Gene Collection (MGC), Bethesda, MD 20892-2590, USA			
NIH-MGC Project URL: http://mgc.nci.nih.gov			
Contact: MGC help desk			
Email: mgc@bbs.fda.gov			
Tissue Procurement: Baylor Human Genome Sequencing Center			
cDNA Library Preparation: Baylor Human Genome Sequencing Center			
DNA Sequencing by: Baylor College of Medicine Human Genome			
Sequencing Center			
Center code: BCM-HGSC			
Web site: http://www.hgsc.bcm.tmc.edu/cdna/			
Contact: amg@bcm.tmc.edu			
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louissege, H.,			
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Manavati,			
A.N., Gibbs, R.A.			
Clone distribution: MGC clone distribution information can be found			
through the I.M.A.G.E. Consortium/ILN at: http://image.llnl.gov			
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Db      217  GACACAAAGCCTCGAATGATGCTGCTGCTCGCATTTGCTAAGACTTATCTGGAC 276
Qy      61  ArgValPheLyAsnTyRgIntnThProaRphIsTyRThLeuArgLySleSerLeu 80
Db      277  AGGGTATTTAAACCAACAGAGACCCCTGACATTATATCTCCGGAAGATCAGACACCTC 336
Qy      81  AlaAsnSerPheLeuThrIleTyRLeuTyRAspLeuArgLeuCyHisAlaHisMetThrCyS 100
Db      337  GCCAATTCCTTTTACATCAAGAGAGACCTCCGGCTCTGTATGCCACATGACATGCG 396
Qy      101  HisCyGlyGluGluAlaMetLySlyTyRSerGlnIleLeuSerHisPheGluTySLeu 120
Db      397  CATTGTGGGAGGAGCAATGAGAAATACAGCCAGATTCTGAGTCACCTTGAAGAGCTG 456
Qy      121  GluProGlnAlaAlaValValLySAlaLeuGlyGluLeuAspIleLeuLeuGlnTTPMet 140
Db      457  GAACCTCAGACAGACAGTGTGAAAGGCTTTGGGGAACTAGACATCTCTTGCAATGAGATG 516
Qy      141  GluGluThrGlu 144
Db      517  GAGGAGACAGCA 528

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LOCUS Homo sapiens Interleukin 20, mRNA (cDNA clone MGC:96943
DEFINITION IMAGE:7262152), complete cds.
ACCESSION BC069425
VERSION BC069425.1 GI:47479503
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 531)
Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
Collins FS, Wagner L, Shenman CM, Schuler GD, Altschul SF, Zeeberg
B, Bietow KH, Schaefer CF, Bhac NK, Hopkins RP, Jordan H, Moore T,
Max SI, Wang U, Hsieh F, Diatchenko L, Marusina RA, Farmer AA, Rubin
GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
Schectz TE, Brownstein MJ, Ustin TB, Toshiyuki S, Carninci P,
Prange C, Raha SS, Loguellano NA, Peters GJ, Abramson RD, Mullaby
SJ, Bosak SM, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahy J,
Helton E, Kettelman M, Madan A, Rodrigues S, Sanchez A, Whitting M,
Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakeley RW,
Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
Schmutz J, Myers RM, Butlerfield YS, Krzywinski MI, Skalska U,
Mammalian Gene Collection Program Team
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 531)
Director MGC Project.
Direct Submission
Submitted (29-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gcabbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louieged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
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ALGEIDLILQNMETE"

ORIGIN
Alignment Scores:
Pred. No.: 4,73e-72 Length: 531
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
DB: 8 Gaps: 0

US-10-789-251-26 (1-144) x BC069425 (1-531)
Qy      1  CyValIleAlaThraNleuGlnGluIleArgAnGlyPheSerAspIleArgGlySer 20
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Qy      21  ValGlnAlaLyAspGlyAsnIleAspIleArgIleLeuArgRgThrgIuSerLeuGln 40
Db      157  GTGCAAGCCAAAGATGGAACATTGACATCAGATCTTAAGAGGAGCTGAGCTTTGGCA 216
Qy      41  AaPThLyEProAlaAnaRgCyCySLeuLeuArghIsleuLeuArgLeuTyRLeuAaP 60
Db      217  GACACAAAGCCTCGAATGATGCTGCTGCTCGCATTTGCTAAGACTTATCTGGAC 276
Qy      61  ArgValPheLyAsnTyRgIntnThProaRphIsTyRThLeuArgLySleSerLeu 80
Db      277  AGGGTATTTAAACCAACAGAGACCCCTGACATTATATCTCCGGAAGATCAGACACCTC 336
Qy      81  AlaAsnSerPheLeuThrIleTyRLeuTyRAspLeuArgLeuCyHisAlaHisMetThrCyS 100
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Db 397 CATTGTGGGAGAGACATGAAATAACAGCCAGATTCTGAGTCATTGAAAAGCTG 456
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Qy 141 Gtugluthrglu 144
Db 517 GAGGAGACAGAA 528

RESULT 12
BC069449 531 bp mRNA linear PRI 08-MAR-2005
LOCUS Homo sapiens interleukin 20, mRNA (CDNA clone MGC:96955
DEFINITION IMAGE:7262164), complete cds.
ACCESSION BC069449
VERSION BC069449.1 GI:47480911
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 531)
Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
Collins FS, Wagner L, Shenmen CM, Schuler GD, Altshul SF, Zeeberg
B, Buetow KH, Scheffer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
Max SI, Wang J, Haile P, Diatchenko L, Marusina K, Farmer AA, Rubin
MG, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavani JL,
Schetz TE, Brownstein MJ, Ustin TB, Toshimiyuki S, Carninci P,
Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullaly
SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
Richardson S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
Villalón DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fehey J,
Heltson B, Kettman M, Madan A, Rodrigues S, Sanchez A, Whitting M,
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Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
Smalins DE, Schnerch A, Schein JF, Jones SJ and Marra MA.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 531)
Director MGC Project.
Direct Submission
Submitted (29-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing Center
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louieged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

FEATURES
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Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>
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Location/Qualifiers
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CDs
US-10-789-251-26 (1-144) x BC069449 (1-531)

ORIGIN

Alignment Scores:
Pred. No.: 4,73e-72 Length: 531
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
DB: 8 Gaps: 0

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Db 337 GCCAATTCCTTCTTACATCACAAGAGACCTCCGCTCTGTCATGCGCACATGACATGC 396
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Db 457 GAACCTCAGGACAGCAGTTGTGAAGCTTTGGGGAACCTAGACATTTCTTGTGCAATGATG 516
Qy 141 Gtugluthrglu 144
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RESULT 13
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LOCUS BC069487
DEFINITION Homo sapiens interleukin 20, mRNA (CDNA clone MGC:96967
IMAGE:7262176), complete cds.
ACCESSION BC069487
VERSION BC069487.1 GI:47480770

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
CONSRMT
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT

MGC.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 531)
Straussberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
Max SI, Wang J, Haieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
Scheetz TB, Brownstein MJ, Ustin TB, Toshiyuki S, Carninci P,
Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
Villalón DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
Helton E, Kettman M, Madan A, Rodrigues S, Sanchez SJ and Marra MA.
Mammalian Gene Collection Program Team
human and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 531)
Director MGC Project.
Direct Submission
Submitted (29-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: mgc@bcm.tmc.edu
Email: cgabs@bcm.tmc.edu
Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing Center
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: mgc@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegd, H.,
Kowls, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
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Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 4,73e-72 Length: 531
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Beet Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
DB: 8 Gaps: 0
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517 GAGAGACAGACAA 528
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DEFINITION
Homo sapiens interleukin 20, mRNA (CDNA clone MGC:96884
IMAGE:7262093), complete cds.
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VERSION
BC069523.1 GI:47479431
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 531)
Straussberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
Max SI, Wang J, Haieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
Scheetz TB, Brownstein MJ, Ustin TB, Toshiyuki S, Carninci P,
Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
Villalón DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,

Helton B, Kettelman M, Madan A, Rodrigues S, Sanchez A, Whitting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakeley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield JS, Krzywinski MI, Skalska U, Smalhus DE, Schnerch A, Schein JE, Jones SJ and Marra MA. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
PUBMED
12477932

REFERENCE
2 (bases 1 to 531)
Director MGC Project.
Direct Submission
Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Offices, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing Center
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnarathne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Louieged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Navavati, A.N., Gibbs, R.A.

REMARK

COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LML at: <http://lml.gov>
Series: IRBR Plate: 1 Row: a Column: 3.
Location/Qualifiers

FEATURES

source

gene

CDS

ORIGIN

Alignment Scores:

Pred. No.: 4,73e-72 Length: 531
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
Gaps: 0

US-10-789-251-26 (1-144) x BC069523 (1-531)

Qy 1 CyvalleialathrasnleugngluileargAsnglyPheSerapilearglySer 20
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Db 97 TGTGTATGCGCCAAACCTTCGAGAAATCGAATTTCTAGATCCGGGCACT 156
Qy 21 ValGlnAluLysApGlyAsnIleapIleargIleleuArgThrgIuseLeuGln 40
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Db 337 GCCAATTCCTTCTTCCATCAATCAAGAGACCTCGGCTCTGTCATGCCACATGATGC 396
Qy 101 HisCyGlyGluGluAlaMetLysLysTyTserGlnIleuSerHisPheGlyLeu 120
| | | | |
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Db 517 GAGAGACAGAA 528

RESULT 15
BC069559 531 bp mRNA linear PRI 08-MAR-2005
LOCUS
Homo sapiens interleukin 20, mRNA (CDNA clone MGC:96896
DEFINITION
IMAGE:7262105), complete cds.
ACCESSION
BC069559.1 GI:47480991
VERSION
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 531)
Straussberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GP, Altschul SF, Zeeberg B, Buelow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Heien F, Diatchenko L, Narusina K, Farmer AA, Rubin GM, Hong T, Brownstein MJ, Usslin TB, Toshitsuyki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullany SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunnarathne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Huiyk SW, Villalón DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey U, Helton B, Kettelman M, Madan A, Rodriguez S, Sanchez A, Whitting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakeley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield JS, Krzywinski MI, Skalska U, Smalhus DE, Schnerch A, Schein JE, Jones SJ and Marra MA. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
PUBMED
12477932

REFERENCE
2 (bases 1 to 531)
Director MGC Project.
Direct Submission
Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Offices, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT MGC help desk

Email: cgabds-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing Center
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegod, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRBR Plate: 1 Row: B Column: 3.
Location/Qualifiers

FEATURES

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ORIGIN

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Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
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US-10-789-251-26 (1-144) x BC069559 (1-531)

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DB 97 TGTGTGATCGCCCAAACTTCAGAAATCGAAATGGATTTCTGTGATACGAGGACGT 156
QY 21 ValGlnAlaIleAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
DB 157 GTCCAAAGCCAAATGGAAACATTGACATCAAAATCTTAAAGAGAGACTGAATCTTTGCCA 216
QY 41 AspThrIlePheAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 217 GACCAAAAGCTCGAATGATGATGCTGCTCTGGGCAATTTGCTAAGACTCTATCTGGAC 276
QY 61 ArgValPheIleAsnTyrGlnThrProAspHisTyrThrLeuArgGlyIleSerSerLeu 80
DB 277 AGGGTATTTAAAACTACAGACCCCTGACCATTTATCTCTCCGAAAGATCAGCAGCTTC 336
QY 81 AlaAsnSerPheLeuThrIleLeuIleValAspLeuArgLeuCysHisAlaHisMetThrCys 100

DB 337 GCCAATTCCTTCTTACCATCAAGAGACCTCCGGCTCTGTCAATGCCACATGACATGC 396
QY 101 HsCysGlyGluGluAlaMetIleValTyrSerGlnIleLeuSerHisPheGluValLeu 120
DB 397 CATTGTGGGGAGAGAAAGCAATGAAGAAATCAGCCAGATTCTGATCACTTTGAAAAAGCTG 456
QY 121 GIUPROGlnAlaValValIleValIleLeuGlyGluLeuAspIleLeuLeuGlnTyrPhe 140
DB 457 GAACTCAGGACGACGAGTGTGAAAGCTTTGGGGGAACTAGACATTTCTTGCATAGATG 516
QY 141 GIUGIUThrGlu 144
DB 517 GAGGAGACAGAA 528

Search completed: December 28, 2005, 12:45:48
Job time : 2950 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 28, 2005, 11:43:12 ; Search time 499 Seconds
(without alignments)
1923.278 Million cell updates/sec

Title: US-10-789-251-26
Perfect score: 753
Sequence: 1 CVIATNLTGIRNGFSIDIRG.....AVVKALGELDILLQMMETE 144

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNIT=bits -START=1 -END=-1 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEA_SIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_WMAP -LARGEOQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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12: genebegn20088.*
13: genebegn20098.*
14: genebegn20108.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	100.0	528	12	ADM95042 Human int
2	753	100.0	531	14	ADV42800 Human pcy
3	753	100.0	926	2	AAK77692 Human zcy
4	753	100.0	926	9	ACF05161 Polynucle

5	753	100.0	926	10	AAD61821 Human zcy
6	753	100.0	926	10	ADG66668 Human zcy
7	753	100.0	926	12	ADG88066 Human zcy
8	753	100.0	926	13	ADR16327 Human zcy
9	753	100.0	926	13	ADR24325 Breast ca
10	753	100.0	926	13	ADR18362 Human zcy
11	753	100.0	926	14	AEA50048 Human zcy
12	753	100.0	926	14	AEA28786 Full leng
13	749	99.5	462	8	ABV75151 Human int
14	749	99.5	462	14	ABV75151 Human int
15	749	99.5	513	8	ABV75154 BC sequen
16	749	99.5	528	12	ADL15289 Human int
17	749	99.5	867	6	ABO74562 Human Lp8
18	749	99.5	867	6	ABV73092 Human Lp8
19	749	99.5	925	12	ADN12153 Human Lp8
20	746	99.1	926	13	ADG31716 DNA encod
21	746	99.1	926	13	ADG31716 DNA encod
22	739	98.1	1571	3	AAA37138 Human PRO
23	739	98.1	1571	4	AAFS4484 Primer #1
24	739	98.1	1571	4	AAFS21292 Human CDN
25	739	98.1	1571	4	AAFS21516 Human CDN
26	739	98.1	1571	4	AAFS46229 Human DNA
27	739	98.1	1571	4	AAFS2126 Human PRO
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ALIGNMENTS

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ID ADM95042 standard; DNA; 528 BP.
XX
AC ADM95042;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human Interleukin-20 (IL-20) gene SegID4.
XX
KW colon cancer; interleukin 20 receptor alpha chain;
XX IL-20 receptor alpha chain; cytosolic; gene; ds; human.
XX
OS Homo sapiens.
XX
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FT Key Location/Qualifiers
FT CDS 1..528
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FT /partial
FT /note= "No stop codon"
XX
PN JP2004075569-A.
XX
PD 11-MAR-2004.
XX
PF 12-AUG-2002; 2002JP-00234880.
XX

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QY 121 GIUPROGINA1A1A1A1Val1Val1Lys1Ala1Leu1G1Y1G1Leu1Asp1Leu1Leu1G1n1T1P1Met 140
DB 457 GAACCTCAGGACAGCAGTTGTGAAGGCTTGGGGAACTAGACATTCCTTCGCAATGAGATG 516
QY 141 GIUG1U1Th1G1U 144
DB 517 GAGAGACAGAA 528
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ID AAK77692 standard; cDNA; 926 BP.
XX
XX AAK77692;
AC
XX
XX 09-AUG-1999 (first entry)
DT
XX
XX Human Zcyto10 allele 1 cDNA.
DE
XX
XX Zcyto10; four alpha helix cytokine; vulnery; cytostatic; haemostatic;
KW anti-inflammatory; anti-asthmatic; growth factor; maintenance factor;
KW trachea; salivary gland; stomach; pancreas; muscle; gene therapy; cancer;
KW proliferation; differentiation; modulator; gastrointestinal tract;
KW oral cavity; asthma; tracheobronchial tract; bronchitis; wound healing;
KW platelet count; thrombocytopenia; human; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT CDS 45..575
FT /tag= a
FT /product= "Zcyto10"
XX
XX MO9927103-A1.
XX
XX 03-JUN-1999.
XX
XX 25-NOV-1998; 98WO-US025228.
XX
XX 26-NOV-1997; 97US-00979156.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Conklin DC, Haldeman BA, Grosemann A;
PI
XX
XX MPI; 1999-357840/30.
XX
XX P-PSDB; AAY08661.
XX
XX New mammalian cytokine-like polynucleotide useful in the treatment of
XX asthma and bronchitis.
XX
XX Claim 3; Page 63-64; 82pp; English.
XX
XX This invention describes a novel mammalian four alpha helix cytokine
XX designated Zcyto10 which has vulnerary, cytostatic, anti-inflammatory,
XX anti-asthmatic and haemostatic activity. Zcyto10 may be a growth and/or
XX maintenance factor in the trachea and salivary glands, stomach, pancreas
XX and muscle. Zcyto10 polynucleotides are useful as sources of primers and
XX probes, and to determine if the Zcyto10 gene is present on chromosome 1,
XX or to detect any mutations that may have occurred. Zcyto10
XX polynucleotides are also useful as gene therapy reagents. The Zcyto10
XX polypeptide, its fragments, and antibodies, as well as compounds
XX identified as having binding affinity to Zcyto10, should be useful in the
XX development of conditions associated with abnormal physiology or
XX treatment, including abnormal proliferation, e.g. cancerous conditions,
XX or degenerative conditions or altered immunity. The products are also
XX useful for modulating cell proliferation, cell differentiation or
XX cytokine production in the prevention or treatment of conditions
XX characterized by abnormal cell proliferation, cell differentiation or
XX cytokine production. Zcyto10 polypeptides, agonists and antagonists may
```

```
CC be therapeutically useful in the regeneration of the gastrointestinal
CC tract or oral cavity, as well as in the treatment of asthma, and other
CC diseases of the tracheobronchial tract such as bronchitis. Zcyto10
CC polypeptides may also be useful to promote wound healing, and to increase
CC platelet count, e.g. in cancer patients who experience thrombocytopenia
CC due to chemotherapy or radiation therapy
XX
XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.17e-86 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 2 Gaps: 0
US-10-789-251-26 (1-144) x AAK77692 (1-926)
QY 1 CysVal1IleAla1ThrAsnLeuG1nG1U1Lea1GAsnG1Y1PheSerAsp1Lea1Arg1YSer 20
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QY 21 ValG1nAla1LysAspG1YAsn1LeaAsp1Lea1Arg1Leu1Arg1Th1G1nSer1LeuG1n 40
DB 201 GTGCAGGCCAAAGATGGAACATTTGACATCAGAAATTTTAAGAGAGACTAGTCTTGCAA 260
QY 41 AspThr1YsP1Ro1A1Asn1Arg1Cys1Leu1Leu1Arg1H1s1Leu1Arg1Leu1Yr1Leu1Asp 60
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QY 61 ArgVal1Phe1YAsn1YrG1nTh1P1Ro1Asp1H1s1YrTh1Leu1Arg1Yr1Leu1Ser1Leu 80
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QY 101 H1SCYGG1G1UG1U1A1A1Me1Lys1Yr1Ser1G1n1Leu1Ser1H1sPhe1G1u1Lys1Leu 120
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QY 141 GIUG1U1Th1G1U 144
DB 561 GAGAGACAGAA 572
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ID ACF05161 standard; cDNA; 926 BP.
XX
XX ACF05161;
XX
XX 06-NOV-2003 (first entry)
DT
XX
XX Polynucleotide encoding human interleukin-20.
DE
XX
XX Human; interleukin-20; IL-20; cervical cancer; cytostatic; virucide;
KW gene; ss.
XX
XX Homo sapiens.
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XX Key Location/Qualifiers
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FT /tag= a
FT /product= "Human IL-20"
FT sig_peptide 45..116
FT mat_peptide 117..572
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CC oral cavity and for modulating muscle tone in the tracheobronchial tract,
CC and for treating muscle atrophy in the elderly, sick or bed-ridden.
CC Zcyto10 is also useful for promoting wound healing. The present sequence
CC is human zcyto10 cDNA. The zcyto10 gene is located on chromosome 10

XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,17e-86	Length:	926
Score:	753.00	Matches:	144
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-10-789-251-26 (1-144) x ADG61821 (1-926)

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DB 201 GTGCAAGCCAAAGATGGAACATTGACATCAGATCTTAAAGGAGACTGAGCTTTGCAA 260
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAAGCCGCGAATGATGCTGCTCTCGCCATTGCTAAGACTCTATCTGAGAC 320
QY 61 ArgValPheLeuAsnTyrGlnThrProAspHisTyrThrLeuArgGlyIleSerSerLeu 80
DB 321 AGGGTATTTAAATACTACACAGACCCCTGACATTAATCTCCGGAAGATCAGCAGCTTC 380
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QY 101 HisCysGlyGluGlnAlaMetIleuYlsTyrSerGlnIleLeuSerHisPheGluYlsLeu 120
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DB 501 GAACCTCAGCGACGACGCTTGAAGCCTTGGGGGAATGACATCTTCTGCAATGAGATG 560
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DB 561 GAGGAGACAGAA 572
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RESULT 6

ID ADG46668 standard; DNA; 926 BP.

XX ADG46668;

XX 11-MAR-2004 (first entry)

XX Human Zcyto10 DNA #1.

XX cytokine-like polypeptide-10; zcyto10; wound healing;
XX platelet proliferation; wound repair; mucous production; asthma;
XX bronchitis; tracheobronchial tract disease; periodontal disease;
XX skin condition; psoriasis; eczema; dry skin; protein therapy; human;
XX vunerary; respiratory; anti-bronchitic; dental; dermatological; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

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XX US2003176657-A1.

XX 18-SEP-2003.

XX 15-APR-2003; 2003US-00413661.

XX 26-NOV-1997; 97US-0066597P.

XX 25-NOV-1998; 98US-0019598P.

XX 17-MAY-1999; 99US-00313458.

XX (CONK/) CONKLIN D C.

XX (HALD/) HALDEMAN B A.

XX Conklin DC, Haldeman BA;

XX WPI: 2003-86365/80.

XX P-PSDB; ADG46669, ADG46679.

XX Novel isolated mammalian cytokine-like polypeptide-10 (Zcyto10), useful

XX for treating asthma, bronchitis and other tracheobronchial damage.

XX Disclosure; SEQ ID NO 1; 31pp; English.

XX The present invention relates to novel mammalian cytokine-like

XX polypeptide-10 (Zcyto10) proteins and polynucleotides encoding such

XX proteins. Sequences of the invention are useful for promoting the healing

XX of wounds and for stimulating the proliferation of platelets in

XX particular Zcyto10 polypeptides may be used in trachea-specific or

XX tracheobronchial-specific applications such as maintenance or wound

XX repair of the tracheobronchial epithelium or cells underlying it; in

XX regulating mucous production; mucociliary clearance of debris; in

XX treatment of asthma, bronchitis and other diseases of the

XX tracheobronchial tract. They are also used to promote regeneration of

XX affected tissues which may be especially useful in the treatment of

XX periodontal disease. Zcyto10 polypeptides can be used to treat skin

XX conditions such as psoriasis, eczema and dry skin in general. They are

XX also used in protein therapy. The present sequence is human zcyto10 DNA.

XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,17e-86	Length:	926
Score:	753.00	Matches:	144
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-789-251-26 (1-144) x ADG46668 (1-926)

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DB 141 TGTGTGATCGCCACAAACCTTCAGAAATACGAAATGATTTTCTGACATACGGGGCAGT 200
QY 21 ValGlnAlaLeuAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
DB 201 GTGCAAGCCAAAGATGGAACATTGACATCAGATCTTAAAGGAGACTGAGCTTTGCAA 260
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAAGCCGCGAATGATGCTGCTCTCGCCATTGCTAAGACTCTATCTGAGAC 320
QY 61 ArgValPheLeuAsnTyrGlnThrProAspHisTyrThrLeuArgGlyIleSerSerLeu 80
DB 321 AGGGTATTTAAATACTACACAGACCCCTGACATTAATCTCCGGAAGATCAGCAGCTTC 380
QY 81 AlaAsnSerPheLeuThrIleIleuYlsAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 381 GCCATTCTCTTCTTACCATCAAGAAAGACCTCCGGCTCTGTCATGCCACATGACATGC 440
```

```
QY 101 HICSGYGLVGLUJLALAMETLYSLYSTRSERGLNILEUSERTHSPHEGLULYSLEU 120
    |||
DB 441 CATTTGGGGAGAGAACCAATGAAGAAATACAGCCAGATTCTGAGTACTTTGAAAAGCTG 500
QY 121 GLUPROGLNALALAVAlVAllySAlALeUGLyGLULeUASpIleUleUGInTPMeC 140
    |||
DB 501 GAACCTCAGGACGACATTTGTGAAGGCTTTGGGGAACTAGACATTTCTTGCATGTGATG 560
QY 141 GLUGLUThrGlu 144
    |||
DB 561 GAGAGACACAGAA 572
RESULT 7
ADQ88066
ID ADQ88066 standard; DNA; 926 BP.
AC ADQ88066;
XX
XX
DT 07-OCT-2004 (first entry)
XX
DE Human Zcyto10 longer form DNA.
XX
Mammalian cytokine-like polypeptide-10; Zcyto10; cell proliferation;
KW cell differentiation; cytokine production; autoimmune disease;
KW insulin dependent diabetes mellitus; multiple sclerosis;
KW rheumatoid arthritis; cancer; wound healing; tissue regeneration;
KW platelet count; asthma; skin disease; psoriasis; eczema; dry skin;
KW antidiabetic; neuroprotective; antirheumatic; cytostatic;
KW immunostimulant; vulnary; antiasthmatic; antipsoriatic; dermatological;
KW gene therapy; human; gene; ds.
XX
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 45..575
    /*tag= b
    /product= "Human Zcyto10 protein"
FT sig_peptide 45..116
    /*tag= a
    /*tag= c
    /product= "Human mature Zcyto10 protein"
FT mat_peptide 117..572
    /*tag= c
    /product= "Human mature Zcyto10 protein"
FT CDS 141..575
    /*tag= d
    /product= "Human Zcyto10 protein fragment"
    /partial
    /note= "No start codon"
XX
XX
PN US2004142428-A1.
XX
PD 22-JUL-2004.
XX
PF 27-FEB-2004; 2004US-00789129.
XX
PR 26-NOV-1997; 97US-0066597P.
PR 25-NOV-1998; 98US-00199586.
PR 15-APR-2003; 2003US-00413661.
XX
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Conklin DC, Haldeman BA;
XX
XX
DR MPI; 2004-552564/53.
DR P-PSDB; ADQ88067, ADQ88077, ADQ88091.
XX
XX
PT New Zcyto10 polypeptides and polynucleotides, useful for treating
PT autoimmune diseases (e.g. insulin dependent diabetes mellitus, multiple
PT sclerosis or rheumatoid arthritis), or skin conditions (e.g. psoriasis or
PT eczema).
XX
XX
PS Disclosure; SEQ ID NO 1; 31pp; English.
XX
```

```
CC The present invention provides mammalian cytokine-like polypeptide-10
CC (Zcyto10) proteins and their encoding polynucleotides. The invention is
CC useful for treating conditions characterised by improper cell
CC proliferation, cell differentiation or cytokine production, specifically
CC for treating autoimmune diseases such as insulin dependent diabetes
CC mellitus, multiple sclerosis and rheumatoid arthritis and for inhibiting
CC cancer cell growth. The invention is also used to stimulate the immune
CC system, to enhance wound healing and promote regeneration of affected
CC tissues, to increase platelet count and to treat asthma and skin
CC conditions such as psoriasis, eczema and dry skin. The invention acts as
CC an antidiabetic, neuroprotective, antirheumatic, antiarthritic,
CC cytostatic, immunostimulant, vulnary, antiasthmatic, antipsoriatic and
CC dermatological agent. The invention is also used in gene therapy. The
CC present sequence is human Zcyto10 longer form DNA.
XX
SQ Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1.17e-86 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
XX
US-10-789-251-26 (1-144) x ADQ88066 (1-926)
QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 141 TGTGTGATGTCGACAAACCTTCAGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200
QY 21 ValGlnAlaIleAspGlyAsnIleAspIleArgIleLeuArgThrGluSerLeuGln 40
DB 201 GTGCAGGCCAAAGATGGAACAATTGACATCAAAATCTTAAAGAGACTAGTCTTTGCCAA 260
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuIleuAsp 60
DB 261 GACACAAAGCCCTGCGATGATGCTGCCCTCCGCGCATTTGCTGAAGCTATCTGGAGC 320
QY 61 ArgValPheLeuAsnIleGlnThrProAspHisIleThrLeuArgIleSerSerLeu 80
DB 321 AGGGATATTTAAAACTACACAGACCCCTGACCATTTATCTCTCGGAAAGATCAGCACCCCTC 380
QY 81 AlaAsnSerPheLeuThrIleLeuIleAspLeuArgLeuCysHisIleHisMetThrCys 100
DB 381 GCCAATCTCTTCTTACCATCAAGAGAGACTCCGCTGTGATGCCACATGACATGC 440
QY 101 HICSGYGLVGLUJLALAMETLYSLYSTRSERGLNILEUSERTHSPHEGLULYSLEU 120
DB 441 CATTTGGGGAGAGAACCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500
QY 121 GLUPROGLNALALAVAlVAllySAlALeUGLyGLULeUASpIleUleUGInTPMeC 140
DB 501 GAACCTCAGGACGACATTTGTGAAGGCTTTGGGGAACTAGACATTTCTTGCATGTGATG 560
QY 141 GLUGLUThrGlu 144
DB 561 GAGAGACACAGAA 572
RESULT 8
ADRI6327
ID ADRI6327 standard; DNA; 926 BP.
XX
XX
AC ADRI6327;
XX
XX
DT 21-OCT-2004 (first entry)
XX
DE Human cytokine-like polypeptide-10 (Zcyto10) long form DNA.
XX
KW Cytokine-like polypeptide-10; Zcyto10; therapy; asthma; infection;
KW psoriasis; eczema; dry skin; wound healing; platelet proliferation;
KW human; gene; ds.
XX
```

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OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 45..575
FT /tag= b
FT /product= "Zcyto10 long form protein"
FT sig_peptide 45..116
FT /tag= a
FT mat_peptide 117..572
FT /tag= c
FT /product= "Mature Zcyto10 long form protein"
XX
XX US2004152878-A1.
XX
XX PD 05-AUG-2004.
XX
XX PF 27-FEB-2004; 2004US-00789968.
XX
XX PR 26-NOV-1997; 97US-0066597P.
XX PR 25-NOV-1998; 98US-00199586.
XX PR 15-APR-2003; 2003US-00413661.
XX
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Conklin DC, Haldeman BA;
XX
XX DR WPI; 2004-580197/56.
XX DR P-PsDB; ADR16338, ADR16338.
XX
XX PT New isolated antibody that binds to a Zcyto10 polypeptide, useful for
XX PT treating asthma, microbial or viral infections, and for promoting the
XX PT healing of wounds, psoriasis, eczema or dry skin.
XX
XX PS Disclosure; SEQ ID NO 1; 32pp; English.
XX
XX CC The invention relates to novel cytokine-like polypeptide-10 (Zcyto10)
XX CC polypeptides and polynucleotides. Zcyto10 sequences are useful for
XX CC treating asthma, microbial or viral infections, psoriasis, eczema or dry
XX CC skin, for promoting the healing of wounds and for stimulating the
XX CC proliferation of platelets. The present sequence is human Zcyto10 DNA.
XX
XX SQ Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1,17e-86 Length: 926
XX Score: 753.00 Matches: 144
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 13 Gaps: 0
XX
XX US-10-789-251-26 (1-144) x ADR16327 (1-926)
XX
XX QY 1 CysVal11eAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAsp11eArgGlySer 20
XX DB 141 TGTGTGATGCCCAAACTTCAGGAAATACGAAATGATTTTCTGACATACGGGCACT 200
XX
XX QY 21 Val1GlnAlaLeuAspGlyAsn11eArg11eLeuArgGlyThrGlnSerLeuGln 40
XX DB 201 GTGCAAGCCAAAGATGGAACATTGACATCAGAACTTAAAGAGAGACTGAGCTTTGCAA 260
XX
XX QY 41 AAPTThlVpRAlaAsnArgCysCysLeuLeuArgHis1eLeuLeuArgLeuTyrLeuA 60
XX DB 261 GACACAAAGCCGTGGATGATGCTGCTGCGGCATTTGCTAAGACTTATATCTGAGC 320
XX
XX QY 61 ArgValPheLeuAsnTyrGlnThrProAspHisTyrThrLeuArgGlyHisSerSerLeu 80
XX DB 321 AGGGTATTAAACCTACCAAGACCCCTGACATTAATCTCTCGGAAGATCAGCAGCCTTC 380
XX
XX QY 81 AlaAsnSerPheLeuThr11eLeuValAspLeuArgLeuCysHisAlaHisMetThrCys 100
XX DB 381 GCCAATTCTTCTTACATCAAGAGAGACTCGGCTCTGTCATGCCCATGACATGACATGC 440

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QY 101 HisCysGlyGluGluAlaMetLysTyrSerGln11eLeuSerHisPheGluTyrLeu 120
DB 441 CATTGTGGGAGAGAACCAATGAAAGAAATACAGCAATTTCTGATCTTGAAGAGCTG 500
XX
XX QY 121 GluProGlnAlaAlaVal11eArg11eLeuAsp11eLeuLeuGlnTyrMet 140
XX DB 501 GAACCTCAGGACAGCACTTGTGAAGCTTTGGGGAACTAGACATCTTCTGCAATGATG 560
XX
XX QY 141 GlnGluThrGlu 144
XX DB 561 GAGAGACAGAA 572
XX
XX RESULT 9
XX ADR24325
XX ID ADR24325 standard; DNA; 926 BP.
XX
XX AC ADR24325;
XX
XX DT 21-OCT-2004 (first entry)
XX
XX DE Breast cancer prognosis marker #186.
XX
XX KW de; breast cancer; prognosis; gene expression; diagnosis.
XX
XX OS Homo sapiens.
XX
XX PN WO2004065545-A2.
XX
XX PD 05-AUG-2004.
XX
XX PF 15-JAN-2004; 2004WO-US001100.
XX
XX PR 15-JAN-2003; 2003US-00342887.
XX
XX PA (ROSE-) ROSETTA INPHARMATICS LLC.
XX PA (NECA-) NETHERLANDS CANCER INST.
XX
XX PI Van't Veer LJ, He Y;
XX
XX DR WPI; 2004-593473/57.
XX
XX PT Classifying a breast cancer patient according to prognosis comprises
XX PT determining the similarity between the level of expression of each of
XX PT five genes in a cell sample taken from patient, to control levels.
XX
XX PS Disclosure; SEQ ID NO 186; 226pp; English.
XX
XX CC The invention relates to a method of classifying a breast cancer patient
XX CC according to prognosis by determining the similarity between the level of
XX CC expression of each of five genes for which markers are listed in the
XX CC specification, in a cell sample taken from the breast cancer patient, to
XX CC control levels of expression for each respective five genes to obtain a
XX CC patient similarity value. The methods are useful for classifying a breast
XX CC cancer patient according to prognosis. Kits and computer program products
XX CC are useful for data analysis using the diagnostic, prognostic and
XX CC statistical methods of the invention. This sequence corresponds to a
XX CC marker used in the method of the invention.
XX
XX SQ Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1,17e-86 Length: 926
XX Score: 753.00 Matches: 144
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 13 Gaps: 0
XX
XX US-10-789-251-26 (1-144) x ADR24325 (1-926)
XX
XX QY 1 CysVal11eAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAsp11eArgGlySer 20
XX DB 141 TGTGTGATGCCCAAACTTCAGGAAATACGAAATGATTTTCTGACATACGGGCACT 200

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```
QY 21 ValGlnAlaIyAspGlyAsnIleAapIleArgIleLeuArgArgThrGluSerLeuGln 40
DB 201 GTGGCAAGCCAAAGATGAAACATTTGACATCAGAAATCTTAAAGAGAGCTGAGCTTTTGCA 260
QY 41 AapThrLySProAlaAsnArgCySvLeuLeuArgHisleuLeuArgLeuTyrlleuAap 60
DB 261 GACACAAAGCCTGCGAATGATGCTGCTGCTGCGCATTTGGCTTAAGACTTATCTTGAGAC 320
QY 61 ArgValPheLyAsnTyrlleuThrProAspHisTyrlleuArgLySileSerSerLeu 80
DB 321 AGGGATTTTAAATAACACAGAGACCCCTGACATTATATCTCCGGAAGATCAGCAGCCCTC 380
QY 81 AlaAsnSerPheLeuThrIleLySlyAspLeuArgLeuCyHisIleAsIleMetThrCys 100
DB 381 GCCAATTCCTTTCTTTCATCAAGAAAGACCTCCGCTCTGTATGCCCATGACATGAC 440
QY 101 HisCySgIyGluGluAlaMetLySlyTyrsSerGlnIleLeuSerHisPheGluTyrlleu 120
DB 441 CATTGTGGGGAGAGACATGAAAGAAATACAGCCCAATTCCTGATCACTTTGAAAAAGCTG 500
QY 121 GluProGlnAlaAlaValValIySAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
DB 501 GAACCTCAGGACAGCAGATTGTGAAGCTTTGGGGAACTAGACATCTCTGCAATGAGATG 560
QY 141 GluGluThrGlu 144
DB 561 GAGGAGACAGAA 572

RESULT 10
ADSI8362
ID ADSI8362 standard; DNA; 926 BP.
AC ADSI8362;
XX
XX 02-DEC-2004 (first entry)
XX
DE Human Zcyto10 protein encoding DNA #1.
XX
KW Zcyto10; cytokine-like polypeptide; cell proliferation;
KW cell differentiation; autoimmune disease; diabetes; multiple sclerosis;
KW rheumatoid arthritis; asthma; psoriasis; cancer; wound; gene therapy;
KW immunosuppressive; antidiabetic; neuroprotective; antineumatic;
KW antiahrific; antiaesthetic; antipsoriatic; cytostatic; vulnerary;
KW human; gene; chromosome 1q32.2; ds.
XX
XX Homo sapiens.
XX
OS
XX
XX Key Location/Qualifiers
FH CDS 45..575
FT /*tag= b
FT /product= "Zcyto10 protein "
FT sig_peptide 45..116
FT /*tag= a
FT mat_peptide 117..572
FT /*tag= c
FT /product= "Mature Zcyto10 protein"
XX
XX US2004181040-A1.
XX
XX 16-SEP-2004.
XX
XX 29-DEC-2003; 2003US-00748484.
XX
XX 26-NOV-1997; 97US-0066597P.
XX 25-NOV-1998; 98US-00199586.
XX 15-APR-2003; 2003US-00413661.
XX
XX (CONK/) CONKLIN D C.
XX PA (HALD/) HALDEMAN B A.
XX PA (GROS/) GROSSMANN A.
XX
XX Conklin DC, Haldeman BA, Grossmann A;
PI
```

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XX
XX MPI; 2004-667683/65.
DR P-PDB; ADSI8363, ADSI8373.
XX
XX PT New antibody that selectively binds to a Zcyto10 polypeptide useful for
XX PT modulating cell proliferation, cell differentiation or cytokine
XX PT production in the prevention or treatment of e.g. autoimmune diseases,
XX PT cancer or wounds.
XX
XX PS Disclosure; SEQ ID NO 1; 31pp; English.
XX
XX CC The present invention relates to a mammalian cytokine-like polypeptide,
XX CC Zcyto10 and its encoding polynucleotide. The invention is useful for
XX CC modulating cell proliferation, cell differentiation or cytokine
XX CC production in the prevention or treatment of conditions such as
XX CC autoimmune diseases (e.g. diabetes, multiple sclerosis, rheumatoid
XX CC arthritis, asthma or psoriasis) and cancer or wounds. The invention is
XX CC also useful in gene therapy. The present sequence is the human Zcyto10
XX CC protein encoding DNA. This Zcyto10 gene is located on chromosome 1q32.2.
XX
XX
XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.17e-86 Length: 926
XX Score: 753.00 Matches: 144
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 13 Gaps: 0
XX
XX US-10-789-251-26 (1-144) x ADSI8362 (1-926)
XX
XX QY 1 CysValIleAlaIleThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
XX DB 141 TGTGTGATCGCCACAAACCTTCAGAAATGAGAAATGATTTCTGACATACGGGGCAGT 200
XX
XX QY 21 ValGlnAlaIyAspGlyAsnIleAapIleArgIleLeuArgArgThrGluSerLeuGln 40
XX DB 201 GTGGCAAGCCAAAGATGAAACATTTGACATCAGAAATCTTAAAGAGAGCTGAGCTTTGCA 260
XX
XX QY 41 AapThrLySProAlaAsnArgCySvLeuLeuArgHisleuLeuArgLeuTyrlleuAap 60
XX DB 261 GACACAAAGCCTGCGAATGATGCTGCTGCTGCGCATTTGGCTTAAGACTTATCTTGAGAC 320
XX
XX QY 61 ArgValPheLyAsnTyrlleuThrProAspHisTyrlleuArgLySileSerSerLeu 80
XX DB 321 AGGGATTTTAAATAACACAGAGACCCCTGACATTATATCTCCGGAAGATCAGCAGCCCTC 380
XX
XX QY 81 AlaAsnSerPheLeuThrIleLySlyAspLeuArgLeuCyHisIleAsIleMetThrCys 100
XX DB 381 GCCAATTCCTTTCTTTCATCAAGAAAGACCTCCGCTCTGTATGCCCATGACATGACATG 440
XX
XX QY 101 HisCySgIyGluGluAlaMetLySlyTyrsSerGlnIleLeuSerHisPheGluTyrlleu 120
XX DB 441 CATTGTGGGGAGAGACATGAAAGAAATACAGCCCAATTCCTGATCACTTTGAAAAAGCTG 500
XX
XX QY 121 GluProGlnAlaAlaValValIySAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
XX DB 501 GAACCTCAGGACAGCAGATTGTGAAGCTTTGGGGAACTAGACATCTCTGCAATGAGATG 560
XX
XX QY 141 GluGluThrGlu 144
XX DB 561 GAGGAGACAGAA 572
XX
XX
XX RESULT 11
XX AEAS0048
XX ID AEAS0048 standard; cDNA; 926 BP.
XX AC AEAS0048;
XX
XX 11-AUG-2005 (first entry)
XX
XX Full length IL-20 coding sequence.
XX
XX
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XX 88; gene; Antiinflammatory; Gastrointestinal-Gen.; Anticancer;
XX Anticancer; Dermatology; Antiparasitic; Antibacterial;
XX Immunosuppressive; Antimicrobial; IL-Antagonist-20; Interleukin-20;
XX IL-20; Inflammation; Inflammatory bowel disease; ulcerative colitis;
XX Crohn's disease; arthritis; atopic dermatitis; psoriasis; endotoxemia;
XX septicemia; toxic shock syndrome; infectious disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 45..575
XX /*tag= a
XX
XX MO2005052000-A2.
XX
XX 09-JUN-2005.
XX
XX 19-NOV-2004; 2004WO-US039071.
XX
XX 21-NOV-2003; 2003US-0524131P.
XX 24-MAR-2004; 2004US-0555857P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Xu W, Kindsvogel WR, Chen Z, Hughes SD, Chandrasekhar YA;
XX Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
XX
XX WPI; 2005-405360/41.
XX P-PSDB; AEA50049, AEA50050.
XX
XX Producing an antibody to an interleukin-20 (IL-20) polypeptide, useful
XX for treating inflammatory diseases e.g., Crohn's disease, by inoculating
XX an animal with the polypeptide eliciting an immune response to produce
XX the antibody.
XX
XX Example 1; SEQ ID NO 1; 268pp; English.
XX
XX This sequence encodes full length interleukin-20 (IL-20), longer form IL-
XX 20x1. The method of the invention for producing an antibody to IL-20
XX comprises inoculating an animal with an IL-20 polypeptide which elicits
XX an immune response in the animal to produce the antibody, and isolating
XX the antibody from the animal. The antibody is useful for creating a
XX pathological condition in a subject associated with IL-20 activity such
XX as chronic inflammatory condition, specifically inflammatory bowel
XX disease, ulcerative colitis, Crohn's disease, arthritis, atopic
XX dermatitis and psoriasis, or acute inflammatory condition such as
XX endotoxemia, septicemia, toxic shock syndrome and infectious disease. An
XX antagonist of IL-20 is useful for treating a mammal afflicted with an
XX inflammatory disease in which IL-20 plays a role such that the
XX inflammation is reduced, where the antagonist comprises an antibody,
XX antibody fragment, or binding polypeptide that specifically binds a
XX polypeptide or polypeptide fragment of IL-20 or a polypeptide or
XX polypeptide fragment of IL-20, and where the inflammatory activity of IL-
XX 20 is reduced. The method is useful for producing such therapeutic
XX antibody. The antibody or antibody fragment, produced using the above
XX method, binds to IL-20, and inhibits or reduces the pro-inflammatory
XX activity of IL-20. IL-20-induced proliferation or differentiation of
XX hematopoietic cells and hematopoietic cell progenitors may be reduced or
XX inhibited using the antibody.
XX
XX SQ Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.17e-86 Length: 926
XX Score: 753.00 Matches: 144
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 14 Gaps: 0
XX
XX US-10-789-251-26 (1-144) X AEA50048 (1-926)

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QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
Db 141 TGTGTATTCGCCCAAACTTCAGAAATACGAAATGATTTTGTACATACGGGCACT 200
QY 21 ValGlnAlaIleAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
Db 201 GTCCAGACCAAGATGGAACATTTGACATCAGATCTTAAGAGAGACTGAGTCTTTGCAA 260
QY 41 AspThrIleProAlaAsnArgCysGlyLeuLeuArgHisIleLeuArgLeuTyrLeuAsp 60
Db 261 GACACAAAGCTGCGAATGATGCTGCTGCGCATTTGCTAAGACTCTATCTTGAC 320
QY 61 ArgValPheIleAsnTyrGlnThrProAspHisTyrThrLeuArgHisIleSerSerLeu 80
Db 321 AGGATATTTTAAATCACTACAGACCTTGACATTAATCTCTCGGAAGATACAGACCTC 380
QY 81 AlaAsnSerPheLeuThrIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100
Db 381 GCCAATTCCTTCTTACATCAAGAGAGACTCGGCTGTGATGCCACATGACATGCTC 440
QY 101 HisCysGlyGluGluAlaMetIleIleIleIleIleIleIleIleIleIleIleIleIle 120
Db 441 CATTTGGGAGAGAGCAATGAAAGAAATACAGCAATTCGTGACTTTGAAAAAGCTG 500
QY 121 GluProGlnAlaIleValIleValIleValIleValIleValIleValIleValIleVal 140
Db 501 GAACTCAGGACGACGATTTGTGAGGCTTTGGGGAACTAGACATTTCTTCTGCAATGATG 560
QY 141 GluIleThrGlu 144
Db 561 GAGAGACAGAA 572
Db
QY 141 GluIleThrGlu 144
Db 561 GAGAGACAGAA 572
Db
RESULT 12
AEA28786
ID AEA28786 standard; cDNA; 926 BP.
XX
XX AEA28786;
XX
XX 11-AUG-2005 (first entry)
XX
XX Human interleukin 20 (IL-20) precursor cDNA clone.
XX
XX antibody production; cytokine; antiinflammatory; gastrointestinal-gen.;
XX anticancer; antiparasitic; dermatological; antiparasitic; antibacterial;
XX immunosuppressive; antimicrobial; inflammation;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;
XX arthritis; atopic dermatitis; psoriasis; cancer; endotoxemia; sepsis;
XX endotoxemic shock; infectious disease; IL-20; interleukin-20; ss; gene.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 45..575
XX /*tag= a
XX /product= "Human interleukin 20 (IL-20) protein"
XX
XX MO2005052001-A2.
XX
XX 09-JUN-2005.
XX
XX 19-NOV-2004; 2004WO-US039097.
XX
XX 21-NOV-2003; 2003US-0524131P.
XX 24-MAR-2004; 2004US-0555857P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Xu W, Kindsvogel WR, Chen Z, Hughes SD, Chandrasekhar YA;
XX Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
XX
XX WPI; 2005-405360/41.
XX P-PSDB; AEA28787.
XX
XX

```

PT Producing an antibody to an interleukin 20RA (IL-20RA) polypeptide,
PT useful for treating inflammatory diseases e.g., arthritis, by inoculating
PT an animal with the polypeptide which elicits an immune response to
PT produce the antibody.

XX Example 1; SEQ ID NO 1; 265pp; English.

CC The invention relates to a novel method for producing an antibody to a
CC polypeptide. The method comprises inoculating an animal with a
CC polypeptide selected from any of SEQ ID NO: 14, 15, 17 or 19 as given in
CC the specification, where the polypeptide elicits an immune response in
CC the animal to produce the antibody, and isolating the antibody from the
CC animal. The antibody specifically binds to the pro-inflammatory cytokine
CC interleukin 20 (IL-20 or Zcyto10), or one its receptors IL-20RA (Zcytrp7)
CC or IL-20RB (PDIRS1). The method of the invention demonstrates
CC anti-inflammatory, gastrointestinal-gen., antitumor, antiarthritic,
CC dermatological, antiparasitic, antibacterial, immunosuppressive and
CC antimicrobial applications. The antibody may be useful for treating a
CC pathological condition in a subject associated with IL-20RA, such as a
CC chronic inflammatory condition selected from inflammatory bowel disease,
CC ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis and
CC psoriasis, cancer, or an acute inflammatory condition such as
CC endotoxemia, septicemia, toxic shock syndrome and infectious disease. The
CC current sequence is that of a human IL-20 precursor cDNA clone of the
CC invention.

XX SQ Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,17e-86	Length:	926
Score:	753.00	Matches:	144
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-789-251-26 (1-144) x ABA28786 (1-926)

QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 141 TGTGTATCGCCCAAAACCTTCAGAAATCGAAATGGAATTTCTGACATACGGGCGACGT 200
QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB 201 GTGCAGCCCAAGATGAGAAACATTGACATCAGAACTTAAAGGAGACTGAGCTTGGCAA 260
QY 41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAAGCTCGAATGATGATGCTGCTCTCGCCATTGTGTAAGACTTATCTGGAC 320
QY 61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
DB 321 AGGGTATTTTAAACCAACCAAGACCCCTGACATTATATCTCTCCGGAAGATCAGACCCCTC 380
QY 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 381 GCCAAATTCCTTTTACCATCAAGAAAGACCTCCGGCTCTGTATGCCCACATGACATG 440
QY 101 HisCysGlyGluGluIleLysLysLysTyrSerGlnIleLeuSerHisPheGlnLysLeu 120
DB 441 CATTTGGGGAGGAAGCAATGAAAGAAATACAGCCAGATTTGTAGTCACTTGAAGAGCTG 500
QY 121 GluProGlnAlaAlaValValLysValLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
DB 501 GAACCTCAGGCGACAGTGTGAAGGCTTTGGGGAACTAGACATCTCTTGTCAATGGAGT 560
QY 141 GluGluThrGlu 144
DB 561 GAGGAGACAGAA 572

RESULT 13
ABV75151
ID ABV75151 standard; DNA; 462 BP.

XX AC ABV75151;
XX 19-FEB-2003 (first entry)
XX
XX Human interleukin-20 (IL-20) codon optimised fragment zcyto10X1.
XX Protein synthesis; data mining; recombinant; interleukin-20; IL-20;
XX human; ds.
XX Homo sapiens.
XX MO200283853-A2.
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002MO-US011513.
XX
XX 13-APR-2001; 2001US-0283688P.
XX (ZYMO) ZYMOGENETICS INC.
XX Powder TA, Chan C;
XX
XX WPI; 2003-067576/06.
XX
XX New polynucleotide, useful for producing a nucleic acid construct for
XX expression of an amino acid sequence of interest.
XX
XX Example 1; Page 36; 40pp; English.

CC The invention provides a new purified polynucleotide that comprises the
CC nucleic acid sequence A-B-C-D-E; where: A= start codon, B= polynucleotide
CC sequence of 13 nucleic acids, where the sequence has homology with 13
CC base pair (bp) sequence, where at least 5 nucleic acids are identical to
CC a 13 bp sequence (ABV75139), and where the nucleic acid sequence does not
CC code for a stop codon, C= polynucleotide sequence comprising 10, 13, 16
CC or 19 nucleic acids of a 19 bp sequence (ABV75140). D= polynucleotide
CC sequence comprising 8 bp (ABV75141), E= polynucleotide sequence selected
CC from 9 sequences (ABV75144-150) where at least 50% nucleotides are either
CC adenine or thymine, and where only E encodes a stop codon. The
CC polynucleotide is useful for producing a nucleic acid construct for
CC expression of an amino acid sequence of interest. The present sequence
CC represents a human interleukin-20 (IL-20) codon optimised fragment for
CC expression in E. coli

XX SQ Sequence 462 BP; 121 A; 131 C; 117 G; 93 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,38e-86	Length:	462
Score:	749.00	Matches:	143
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.31%	Mismatches:	0
Query Match:	99.47%	Indels:	0
DB:	8	Gaps:	0

US-10-789-251-26 (1-144) x ABV75151 (1-462)

QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 28 TGTGTATCGCCCAACCTTCGACAGGAATCCGTAAGGTTTCTGTAGATCCGTGACAG 87
QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB 88 GTGCAGGCCCAAGATGAGTAAACATTGACATCCGATCTCTCGTACCGAGTCTGCGAG 147
QY 41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 148 GACACCAACCGCGAAGCTGTGCTGCTGCTGCGCCACTGCTGCTGTATCTGGAC 207
QY 61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
DB 208 CGTGTTTTCAAAACCAACCAAGACCCCGGACCACTATACCTGTGTAATCAGCAGCTG 267

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QY      81  AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db      268 GCCAACTCTCTTCTGACCATCAAAAAGACCTGGCTGTGTGTCACGCCCAATGACCTGC 327
QY      101 HisCysGlyGluGluLysMetLysLysTrpSerGlnIleLeuSerHisPheGluLysLeu 120
Db      328 CACTGTGTGAGGAGGACATGAAAAATACAGCCAGATTCTGAGCCACTTCGAAAAACTG 387
QY      121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
Db      388 GAACCCGAGGACAGACGTGTGAAAGCTGTGGTGAACCTGACATTCCTGTCGACGTGATG 447
QY      141 GluGluThrGlu 144
Db      448 GAGGAGACCGAA 459

RESULT 14
ABE26649
ID      ABE26649 standard; DNA; 462 BP.
XX
AC      ABE26649;
XX
DE      08-SEP-2005 (first entry)
XX
DE      Human Interleukin (IL)-20 DNA, SEQ ID NO: 18.
XX
KW      Expression; gene regulation; toxin; interleukin; gene; ds.
XX
OS      Homo sapiens.
XX
FH      Key
FT      CDS
FT      1..462
FT      /tag= a
FT      /product= "Human Interleukin (IL)-20"

MO2005058946-A2.
XX
PD      30-JUN-2005.
XX
XX
PF      10-DEC-2004; 2004WO-US041776.
XX
XX
PR      12-DEC-2003; 2003US-0529412P.
XX
XX
PA      (ZYMO ) ZYMOGENETICS INC.
XX
PI      Chan C, Powder TA;
XX
DR      WPI; 2005-479318/48.
XX
DR      P-PSDB; ABE26650.
XX
XX
PT      New Syn 1 and Syn 2 tight regulated synthetic promoters, useful for
PT      controlling uninduced, leaky expression of proteins that are toxic and
PT      interfere with production of recombinant protein from an Escherichia coli
PT      expression system.
XX
PS      Example 5; SEQ ID NO 18; 39pp; English.
XX
XX
CC      The invention relates to Syn 1 and Syn 2 tight regulated synthetic
CC      promoters and methods for enhancing the expression of recombinant
CC      proteins. The Syn 1 and Syn 2 tight regulated synthetic promoters are
CC      useful for controlling uninduced, leaky expression of proteins that are
CC      toxic and interfere with production of recombinant protein from an
CC      Escherichia coli expression system. They are useful for controlling basal
CC      expression of target genes. The present sequence is the human interleukin
CC      (IL)-20 DNA. This sequence is used in the comparison of promoter
CC      strength.
XX
SQ      Sequence 462 BP; 121 A; 131 C; 117 G; 93 T; 0 U; 0 Other;

```

Alignment Scores: 1.38e-86 Length: 462
Pred. No.: 749.00 Matches: 143
Score:

```

Percent Similarity: 100.00%
Best Local Similarity: 99.31%
Query Match: 99.47%
DB: 14
Gaps: 0
Conservative: 1
Matches: 0
Indels: 0

US-10-789-251-26 (1-144) x ABE26649 (1-462)
QY      1 CysValIleAlaIleThrLeuGlnGlnIleArgAsnGlyPheSerAspIleArgGlySer 20
Db      28 TGTGTATGTGCCCAACCACTGACGAAATCCGTAAACGTTTCTTAGATCCGTGCAGC 87
QY      21 ValGlnAlaLysAspLysAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
Db      88 GTCCAGGCCAAAGATGTAACTTGAATCCGATCTGCTGCTGTCACAGTCTTCGAG 147
QY      41 AspThrLysProAlaIleAsnArgCysCysLeuLeuArgHisIleLeuLeuArgLeuTrpLeuAsp 60
Db      148 GACACCAAAACCGGCGAACCGTTGCTGCTGCTGCGCACCTGCTGCTGCTGTATCTGGAC 207
QY      61 ArgValPheLysAsnTrpGlnThrProAspHisTrpThrLeuArgLysIleSerSerLeu 80
Db      208 CGTGTTCAAAAAATAACAGACACCCGACCACTATACCTGTGTAATAATCAGACACCTG 267
QY      81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db      268 GCCAACTCTCTTCTGACCATCAAAAAGACCTGGCTGTGTGTCACGCCCAATGACCTGC 327
QY      101 HisCysGlyGluGluLysMetLysLysTrpSerGlnIleLeuSerHisPheGluLysLeu 120
Db      328 CACTGTGTGAGGAGGACATGAAAAATACAGCCAGATTCTGAGCCACTTCGAAAAACTG 387
QY      121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
Db      388 GAACCCGAGGACAGACGTGTGAAAGCTGTGGTGAACCTGACATTCCTGTCGACGTGATG 447
QY      141 GluGluThrGlu 144
Db      448 GAGGAGACCGAA 459

RESULT 15
ABV75154
ID      ABV75154 standard; DNA; 513 BP.
XX
AC      ABV75154;
XX
DE      19-FEB-2003 (first entry)
XX
DE      EC sequence upstream of IL-20 codon optimised fragment zcyto10X1.
XX
KW      Protein synthesis; data mining; recombinant; interleukin-20; IL-20;
XX      human; ds.
XX
OS      Synthetic.
XX
OS      Homo sapiens.
XX
PN      WO200283853-A2.
XX
PD      24-OCT-2002.
XX
XX
PF      12-APR-2002; 2002WO-US011513.
XX
XX
PR      13-APR-2001; 2001US-0283688P.
XX
XX
PA      (ZYMO ) ZYMOGENETICS INC.
XX
PI      Powder TA, Chan C;
XX
DR      WPI; 2003-067576/06.
XX
XX
PT      New polynucleotide, useful for producing a nucleic acid construct for
PT      expression of an amino acid sequence of interest.
XX
XX
XX      Example 1; Page 37; 40pp; English.

```

XX The invention provides a new purified polynucleotide that comprises the
CC nucleic acid sequence A-B-C-D-E; where: A= start codon, B= polynucleotide
CC sequence of 13 nucleic acids, where the sequence has homology with 13
CC base pair (bp) sequence, where at least 5 nucleic acids are identical to
CC a 13 bp sequence (ABV75139), and where the nucleic acid sequence does not
CC code for a stop codon, C= polynucleotide sequence comprising 10, 13, 16
CC or 19 nucleic acids of a 19 bp sequence (ABV75140), D= polynucleotide
CC sequence comprising 8 bp (ABV75141), E= polynucleotide sequence selected
CC from 9 sequences (ABV75144-150) where at least 50% nucleotides are either
CC adenine or thymine, and where only E encodes a stop codon. The
CC polynucleotide is useful for producing a nucleic acid construct for
CC expression of an amino acid sequence of interest. The present sequence
CC represents a sequence comprising an expression cassette (EC)
CC polynucleotide sequence inserted upstream of a human interleukin-20 (IL-
CC 20) codon optimised fragment for expression in E. coli
XX

SQ Sequence 513 BP; 143 A; 145 C; 126 G; 99 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,61e-86	Length:	513
Score:	749.00	Matches:	143
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.31%	Mismatches:	0
Query Match:	99.47%	Indels:	0
DB:	8	Gaps:	0

US-10-789-251-26 (1-144) x ABV75154 (1-513)

QY	1	CysValIleAlaThrAsnLeuGlnIleArgAsnGlyPheSerAspIleArgGlySer	20
DB	79	TGTGTATCCGCACCAACCTGCAGGAATCCGTACGGTTCTCTGAGATCCGTGGCAGC	138
QY	21	ValGlnAlaIysAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln	40
DB	139	GTCCAGGCCCAAGATGGTACATTGACATCCGTATCCTGGCTGTAACGAGTCTTGACAG	198
QY	41	AspThrIysProAlaAsnArgCysGlyLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp	60
DB	199	GACACCAAAACCGCGAACCCTGCTGCTGCTGCGCACCTGCTGCTGTAATCGAG	258
QY	61	ArgValPheIysAsnTyrGlnThrProAspHisTyrThrLeuArgIysIleSerSerLeu	80
DB	259	CGTGTTCCTCAAAACCTACAGACCCCGACCACTATACCTCGCTAAATCAGACGCTG	318
QY	81	AlaAsnSerPheLeuThrIleIysIysAspLeuArgLeuCysHisAlaHisMetThrCys	100
DB	319	GCCAACTCCTCTGACCATCAAAAAGACCTGCTGTGTGTCACGCCCATGACCTGC	378
QY	101	HisCysGlyGlnIleuAlaMetIysIysTyrSerGlnIleLeuSerHisPheGlnIysLeu	120
DB	379	CACGTGTGTAGAGAGCAATGAAAAAATACAGCCAGATTCTGAGCCACTTCGAAAAACTG	438
QY	121	GluProGlnAlaIaValIysAlaLeuGlyGlnLeuAspIleLeuLeuGlnTyrMet	140
DB	439	GAACCCGAGGACAGAGGTGAAAGCTCTGGTGAAGTGAACATTCCTGCAAGTGAGT	498
QY	141	GluGlnThrGlu	144
DB	499	GAGGAGACCGAA	510

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Job time : 505 secs